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<p>(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann: Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the

20 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

25 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

30

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.
10
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

20 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30
$$\text{cum } p(\text{ID}) = p(\text{ID}_1)p(\text{ID}_2)p(\text{ID}_3) \dots p(\text{ID}_n)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a
5 Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next
10 generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three additional probe sets. Thus, there are four probes

10 corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by
5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a
10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined a priori, such
15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a
20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the
25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament
30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACCTCCACITGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGTCT
						GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTTGAAAGAGCTTTTGGGATAATGT
WI-7070	226	C T	---		---	TACTAGACTTTATGCCATGGTGTCTTTC/TAGTTTAAATGCTGTCTCTGTCTGTCAG
						AAGCCATTGACGTAAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC(G/C)AA
						AAACACTCTTCTGGGATATCTGCGAGATAGTACCCAAAGATCAGATGCTACCCAGATGTGTTT
						GATAATACATAAGCCCTAGGATTAGATACAATCTTGAAGAAAGAACTGAGACAGATAATCTGAAIT
WI-10744	61	G C	---		---	AAATGAGGTAAAGTTTCAGGCACTCA
						GGGCAAAATACAGGAAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCAAAGGAGGTAGAACA
						TTACAGTAACATATGCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCTAGAATAC/TAGTG
						GGTCCCTAATAGTTATTAGTTCCTTTTCTCCTCTTCTCACTCTGAAATTTATTTTATAGTTAA
WI-9975	126	C T	---		---	GGGATTAGTTACCACCAAAATGTGTATGATCAATTTGATTCITTAAGAA
						GCTAGGTTTGTCTGTGGTGTCTTCACTAGACTGAGATGACTTGATTTACAGTAATCCCTATGT
						GATGTAACCTAGCTAGACCTCCCTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTTCACTGATTAATTTCTCCCAATTAATTCAAAGGGAGTGGACAGGT
WI-8010	247	G T	---		---	CCCTGGCTGAAAAGAAATAAGAGATCCCAAGTGGTGGGG(G/T)CTT
						GCCGGCTATCTTTAAATTTAACTTGATCTTTGGTGTCTTCCATCCTAGGATTCGCCITATAAT
						CTTTGTCTGTCTGTATG/C/ATTACCTGATTCATCTTTTGATACACAAAGGCTGATGGCTCACAATGT
						AGTAGGCCAAATCTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	G C	---		---	TCTCGACTCTATAACAACCTCCAAACAGAA
						GCCCGGCTATCTTTAAATTTAACTTGATCTTTGGTGTCTTCCATCCTA(G/C)GATTCGCCITAT
						AATCTTTGCTCTGTCTGTAGATTACCTGATTCATCTTTTGATACAAAGGCTGATGGCTCACAATGT
						AGTAGGCCAAATCTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	G C	---		---	TCTCGACTCTATAACAACCTCCAAACAGAA
						TATGCACCTCCACAAAAGCGATATAATTTAAAGTTTTTTCATTAGAAATAAATGTATAAAATAA
						ATATGTTATTATAGGCATTTATTACTAACTATAGTCTCTTGGAAAGGAACACCCCAACCAATACCT
						ATAAAGTACATGTAAATTTATAGTAACATATTTTACTATATACATATGGAATAATCATATTCACACA
WI-8007	242	C A	---		---	GAAGAGCTGAACAGACATTCACCGGATACGACTGTGTGGAC(G/A)AGCTGCTG
						TCAGTTGCAAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTTTGTAG
						TCTATATTCACACATATGAGTGAAATTTTC/TGGGGCATGGGAAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCCCAACAATGTATAAGAAATCCCTTTGTTTTAC
WI-9823	97	C T	---		---	ATGCTTCCCAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---			TCCTACATCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCCTGGAATTCCTTCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCTCAJATJGGGGAGCTTGCAAGCCTCCCTTTAGAC ACCTACAGGTACAGCCGACCATGCCCTACCTCCATGCCATGCCAGGGACCCCTTATAGGCCCTCTG TCCTTAACCTGTATGGTATATTAATCCTTGGTGTGGATGTCCTC
WI-9651	139 T C ---			TCCTACATCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCCTGGAATTCCTTCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCTCAJGGGGAGCTTGCAAGCCTCCCTTTAGACACCT CTCJACAGGTACAGCCGACCATGCCCTACCTCCATGCCATGCCAGGGACCCCTTATAGGCCCTCTGT CTTAAACCTGTATGGTATATTAATCCTTGGTGTGGATGTCCTC
WI-7676b	309 A C ---			GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTTCTTGGTGGCTGCTGGGTGCAGGGGAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---			GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCTGGCTTCTTGGTGGCTGCTGGGTGCAGGGGAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---			CATTATCTGTCTGGTCTGTTCATTCATCTCCTCCTCCTCCATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGATTTTGAATATTTTGTGJGJGACTCCTATGCACATGATAAATTTGTTA TGCTGTCTCTATCTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42 T C ---			TTGGTGTGAACCTCAGAAATAGGAAATAAGACAATTTGAJTA/CJGTACCCAGGAAACAAGAG CCCTGCACCTTGACTCCAAAGGAGTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAAGACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---			GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATT CAGGGCTTGCATGCGCTCTATCCCTCTGCTCTC/CJACACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ---			ATAAACCTTGTGTATGTATCACCACCACTCAATTTATCACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAAATCCTAAACATCAATACCTTTCATCCATAAAAATGTCAGCATTT /CJATTAATAAACATAAATTTTAAAGAAAACATAAGGACACATTTTCAAAATTAATAAAAATAAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGAATCATGCTAG

WI-10826	132 A C ---	---	TCCTATTGCAATTCACAGTAGCCCATGAAGTAGGTATAACCAAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAAGCAAGACCTGCAJ/C JCCCTGGCTTCCCTGACTCCAAAGCTTATCCCTTCTCATGTCTGTGTCAGCCAGGACCCCATGCGCA GAAAGCCACGCTCTCCATCCCCAC .
TIGR- A004S25	145 G A ---	---	AGATCGCCATTAGTATTATTCCTTTGAAGATACITTTGGAGATTCAATTTTCTTGAGTGGCACTGCAT GCTCATTGAGTGAAGAACTTTGCGGTATAGAAATGGAATGGAGATTTCAAACAGCTTTGCTGAAAC TGTACTTTGGG/GJCTCCAGACTTCACTGCTCCTTAGGCATTGAACCATCACCTGGTTTGCACTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACAGAAATCATCAAGCAC/AJATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAAGTAACCTCGAAATAGTAGGATAGTATTATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAATTTTCATTCTATGGAACCTCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCAGTAGGAATAAGAACACTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTATAGATAAGGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGAGCGGATT AT[G/A]TCTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACACGCTTTTATGGCACTTCTGGCTCCCTCGTCCAGGAAGATTCTACCTTACCCGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGGGAGGAATCAAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178 G A ---	---	TCAACACGCTTTTATGGCACTTCTGGCTCCCTCGTCCAGGAAGATTCTACCTTACCCGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT

WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTGCTCTAAATGCTACTACAGCCACTGACATGGTTGGCTGGAAATTTCTCTTTAAATGTGGCATATAGGTTTGTGACACAAGAAGTCATACCTTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAAGTGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACAG
WI-9443	211	G A	---	---	TTAAAAACAGTTTCAGGTGGTGAAGCAGAAAAAGGATGTGATTACAATTTAAATGAATCAGTCACATTGCACAAATTAATCCTTTGGCATCATACAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGACCAACACTCATGGAAGGAGTCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCAACCCACTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCACATGCCACATT
WI-7166	59	C T	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGATCATCAACAAGATTTCCTTGTGCAAAATATTTGACTATTCTGTATCTTTCATCCTTGACTAAATTCGTGATTTTCAAGCAGCATCTTCTGGTTTAAACTTGTTTCTGTGAACAATTTGTGAAAGAGTCTTCCCAATTAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C	---	---	GCCTCTCCCCAGGAAGCGGGGCTTGGCCTGGAACTTCCAGAGAGGAGGGGAGCAATTTTAGCCCCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCTGGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT[C/T]GGGGGAGCAGAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCAACCTTCCCCCTGGAGCTC
WI-7259	188	G T	---	---	GCCTCTCCCCAGGAAGCGGGGCTTGGCCTGGAACTTCCAGAGAGGAGGGGAGCAATTTTAGCCCCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCTGGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACACAG[C/C, T]TTGGGGGAGCAGAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCAACCTTCCCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCCTGTGGAGGGTGGCAATTTAGTGGTGACCCCTGCACCAGGGTTTCTAACAGATGACCCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTGACATTTGCCCTCTCACCCCTATATGGCATAACTGCCTAAGCACTCAGGCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGAAGCACTCTGGTTCTCTATCCCCCTGTACATAGAGAGTTTGTATGGGGCCTCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTGT[C/T]TTTCTCCCTCTGGATCAAGTAGGCAGGACATGGGACCAGGTCTGGAGCTGAGCCCTCAGCTGTACTCTCCGAAAAATCCTCTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTCTCTCCCTCTCCCTGCGGACTCTGGGTGAGCTGTGGCTCAGTCCCGCCCAACAGATGCTTTTCTGTCTC
WI-563	87	G A	---	---	TGTGACCAATTTGTTATTTAGAGGGTTTAAACAATGGCCTGACTATCACCTGATGGTGGCCAGAAATTCCTGGGGGAGGGCCTCCCTTGAJCCCTGATCATGTCTACCTAAGTGCCTACTCTAACAATACTACTCCGTGTGGTATGGGATCCTAAGCCCAAAAGCTGAAATGAACATGTTCTAGCAGTACAGAAATCCATACTGCCCTCAGTAAAGGCAAAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191	C A	---			GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATGTCCAAAAAGGC[C/A]CGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	A G	---			GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCT[AG]TCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	A G	---			GACCAGGGCACCAGAAAGCCACGGAAGCCAC[AG]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	C T	---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-10870	103	G A	---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGGCACCTACTTAGA[GA/C]AGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-7719b	281	T C	---			AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATCTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCC[AG]TTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G	---			AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATCTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCC[AG]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A	---			GCCTGGAGTATATCTAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTTTCTTTTGTGA TGCCATTTGAGGGATGATGTTCTTAAACTATGAAGTACTGGCTGCTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94	C G	---	---	TCCCTTTATGCAACCAAGAGATATTTAATAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TGAGGTGGAACTATGCAGTGTCTCGGCCACACA TCCTGCTGGGCCCTACCTGCCCAATTCATCTGCCAATAATCTGCTCTATTGTTGTCATCCTG GAGAATTGAAGGGGAGGTCAGTGTGTTGTCATGATTTGTCAGAGAACCT
WI-7842	57	T C	---	---	CACAGCCATGCCCTTGAGGAGCGGCCACCAGATGCTGAATCCCCTATCCCATTCTGTCGTATGAG TCCGATTTGCCCTTGCAATTAGCATCTGTCTCCCCCAAAAAGAAATGCTATGAAGCTTTCTTTCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145	A C	---	---	CTGCCATCAGCCCACTGGAGTCCACACTTGAATTTGGCAGCTACCACGGGTGCCATGCTCTGG AGGAGAAAGGGGGCCACATCCCAACCCAGCTGTACCAAGCCCGGGAGGTGCAGCCCTTCTCTCC TGCTCTG[C/A/C]TCTGACTCTCTTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTTGTTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGGCTGGGGCTCTAGCCCCA
WI-4767b	173	C A	---	---	TTCCAGTCTGTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCCT CAGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGAC[A/C/A]AAATCACTAAGGAAATTCACCTAAGA CTGCTCTAACCCAGAGATTTTAACT
WI-4767	50	A G	---	---	TTCCAGTCTGTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGATT CCTCAGGTCGGTAAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTTCTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAAATTCACCTAAGAC TCTCTAACCCAGAGATTTTAACT
WI-7718f	222	C T	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAACTATGTATTAAAT
WI-7718e	60	T C	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718d	31	G A	---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATCCAAAGGGGCGTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATCCAAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ACTTTCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTJAGJAT
WI-7718a	42 A T ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTA
WI-7227d	99 G C ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCAATAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCAATAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC GGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAAAGGAGCTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCAATAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCGAGGCATCAATAACAAGCCAGTAGGTACCTGGC TTCCGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGCTGCTCCTGGAGGTGGAGACAAGGAACCTCCG AAGAGGAAGGAAGAAAGCCGCTACTGCTATGTGTGATCCTTCATCGAACAACCTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGGAAGACATGTGCTATTGAATGAGCCCAACACACTGTAAAT ATCCACAGACTCCCTGCCCTGCCCCCATCCCAACJATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGAGACAAGGAACCT/A JCGAAGAGGAAGCAAGAAAGCGTACTGTCTATGTGTGATCCTTCATCGAACAACTGATGCGAA AACTTGAATCTGTACTGAAATGAGGAGAGAGACATGTGCTATTGAAGTGAAGCAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACTACACCCCTTGACCTGGCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCAAGACGGGCTCTGATATCGCTTTGGCATGATTGCAATGGAGGCAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG/A/GJGTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACTACACCCCTTGACCTGGCTGGACTCCTATGATGGCTGCTGJGTGGTTGATAATAA TCAGATCATGCCAAGACGGGCTCTGATAATCGCTTTGGCATGATTGCAATGGAGGCAATGCG GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCACACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTTCTTTCTACC AGCCCTGCAAGTTTCCTCATGGAGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAGATC AGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAGACA AAAGGCTC/GJTGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCACACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCC/GJCTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGAGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCACACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCC/GJCTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGAGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTCCGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGAAATGAACCTCTCTC AGGTACTGACTGTGGGACCAAGAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTAGGTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTCCGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGAAATGAACCTCTCTC AGGTACTGACTGTGGGACCAAGAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTAGGTTTGTCCC

WI-1795b	130 T	C ---	---	GAAGCAACGAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTCTTCCAGACTCTACGATTA AATTGTATGCATGTGAACAACATGATGAGGTACTTAGATCTAGATCTAGTCTGCTTTGCGAAGAAAGATTC/CJC GTCTACCAATTTTACCAAATTTTCGTAGTACAATTTAAGTATCTCTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGCAGGATT
WI-1795a	47 T	C ---	---	GAAGCAACGAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTTC/CJCTCCAGACTCTACGA TTAAATTGTATGCATGTGAACAACATGATGAGGTACTTAGATCTAGTCTGCTTTGCGAAGAAAGAAAGTC GTCTACCAATTTTACCAAATTTTCGTAGTACAATTTAAGTATCTCTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGCAGGATT
WI-10616d	136 G	A ---	---	CACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGCTCTCCATACGTAGGTCTGTCCTCTCTATCACAATTGGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCCAGTCCCTCTCGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 G	A ---	---	CACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGCTCTCCATACGTAGGTCTGTCCTCTCTATCACAATTGGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCCAGTCCCTCTCGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 C	T ---	---	CACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGCTCTCCATACGTAGGTCTGTCCTCTCTATCACAATTGGCCA CGTAGC/CJCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCCAGTCCCTCTCGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 G	C ---	---	CACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGCTCTCCATACGTAGGTCTG/CJCTCTCTATCACAATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCCAGTCCCTCTCGAGACTCCG ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 G	A ---	---	CTCTATTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCAGT/GA/JATACTAATAA AAACCCCTGAAGCTGCTTGCATTTTCAAGATTCAATATATCCAGATTGTTTCCAGCAAGAA AATTTTATTCTCAAGATATAAAAAATAAATAATTTAAATTTTCAGTTTCCTCAAAAGGAATATGAAATT TGTTAAATGCAAAATCCAGCTGTAACTTTTTTGGACTTGTCTTTATTCTT
WI-1126b	230 T	C ---	---	CTCTATTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCAGTACTAATAATAA CCCTGTAAGCTGCTTGCATTTTCAAGATTCAATATATCCAGATTGTTTCCAGCAAGAA TTATTTCTCAAGATATAAAAAATAAATAATTTAAATTTTCAGTTTCCTCAAAAGGAATATGAAATTGTT AAAAATGCAAAATCCAGCTGTAACTTTTTT/CJGGACTTGTCTTTATTCTT

WI-1126a	97	T C	---			CTCTATTCTCTGGGCACCTGCTTCTTTGGGGGCAACCTCCAGTATCACTGATCACTAAATAATAAA CCCTGTAAAGTCTGCTTGCATTTTCAAGATTC/CAATATATATCCAGATTTTCCAGCAAGGAAA ATTTATTCTCAAGATATAAAATAAATAATTTAAATTTCCCTCAAGGAAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTGGACTTGTCTTTATTTCTT
WI-11183c	124	C T	---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACCTTGAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTAGTAATGGAA
WI-11183b	192	T C	---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACCTTGAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATTC/CAATTTGGT ATGTGGTGCTAGAGTAGTAATGGAA
WI-11183a	118	C T	---			TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACCTTGAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAACAA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTAGTAATGGAA
WI-10770b	174	G A	---			GCTTGGTTGCTTTAGTCTATTGCTCAGTCTGAGTTTCCCTTCTGCTGGCCCTTTTGTATTCA CCCATACCTCTATGCCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTTCTTGTACTTTCTCTG TTCACCAACCTTCTTTTATCTTCAGGACACTCA/GA/TTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGCTCCCTTTCCC
WI-10770a	49	G T	---			GCTTGGTTGCTTTAGTCTATTGCTCAGTCTGAGTTTCCCTTCTG/TTGCTGGCCCTTTTGTATT TCACCCATACCTCTATGCCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTTCTTGTACTTTCTC CTGTTCAACCAACCTTCTTTTATCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGCTCCCTTTCCC
WI-9667b	82	C T	---			GATGACAACTTCTGCTGTGACCCCTAGTCCCTGCTCAGTCTGACACTTTTCAATCTCTGCCCTTGTATCGG TTATCACTGGACA/C/TAAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATTCT
WI-9667a	68	G C	---			GATGACAACTTCTGCTGTGACCCCTAGTCCCTGCTCAGTCTGACACTTTTCAATCTCTGCCCTTGTATCGI GCTTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATTCT

WI-10400d	189 A G ---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCTGCTG GTTAACIGTTATAAGATGGTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTAAATTT TGTTCCCTTACCTTTACTCTCCACCCCAAAATAAGTAAGTACCTATGTCAGTGCATGTAG TTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTAAATTT TGTTCCCTTACCTTTACTCTCCACCCCAACAAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTAAATTT TGTTCCCTTACCTTTACTCTCCACCCCAACAAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACCTTTACTCTCCACCCCAACAAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---	AAAGGGCTACAACTAAGGCCAAACCAATGAACGGGTATAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCACCTTAGAAAGGGCATTTCAAGCACATTCATAGAGGCTTCATATACTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACA GTGAATATCCACCTAACGACCTTCTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	AAAGGGCTACAACTAAGGCCAAACCAATGAACGGGTATAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTACCACCTTAGAAAGGGCATTTCAAGCACATTCATAGAGGCTTCATATACTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACAG TGAATATCCACCTAACGACCTTCTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCAGCTTGTGTGCC CAATGAATACTGAGATGCTGGGTGCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAGATCCTGCATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---	CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCAGCTTGTGTGCC CAATGAATACTGAGATGCTGGGTGCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA/CJGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCATTTATGGTGTAGTCTGA

WI-7038a	31	G A	---	---	CGAGCTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTAGATGCTGGGTGCTCTCCCTTCCAGGAATGTCGGGCCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTCTGA
WI-3429b	64	G T	---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGCTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTTCATGTGTCATGTCCTCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTAGAA TCTGACTGTTAAACAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCGGCTCCACACA[C/T]AG CCCTCAGCCCCCTCAGCTTTCATGTGTCATGTCCTCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTAGAA TCTGACTGTTAAACAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATTAAGAGTGAAGTGACGGTACCT GTGAGCCCCATCTTCT[G/A]TGGGATAAGGTGTCCTATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATTAAGAGTGAAGTGACGGTGA CCTGTGAGCCCCATCTTCTGTGGGATAAGGTGTCCTATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATTAAGAGTGAAGTGACGGTGA CCTGTGAGCCCCATCTTCTGTGGGATAAGGTGTCCTATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCTAAACCTTCACTTCCAACTCACTGAAT TTCAATACCTCCATTATTAAATTCATACATCATTTGCAGAGAAAGACACCGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGTATCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAA[T/C]TGAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCTAAACCTTCACTTCCAACTCACTCT GAATTCATATACCTCCATTATTAAATTCATACATCATTTGCAGAGAAAGACACCGGTGCCAACTG GGTTTGGTTGGTGCCTGCACACCCACAGTGGCAACTAAGTGTATCTCTAAA

WI-10613b	172	A C ---	---	---	ATTGTATGCCAAATCATAATACCCTGCATTCTAGAAACATACAGTGTATAGAAATTTGAGCCATA TGGTGAATAATTTAGAAGTATTATCTCTATATGTATATACGTTTAACTCAATGAATGTGATTT TTTGCAACTTTGACAAGGCCAGGCAATTTATTGACGCGCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G A ---	---	---	ATTGTATGCCAAATCATAATACCCTGCATTCTAGAAACATACAGTGTATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACGTTTAACTCAATGAATGTG ATTTTGTCAACTTTGACAAGGCCAGGCAATTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T ---	---	---	GGCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAAGTGACTACCCTTGAAGC ACATCCCTCTGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA[A TJGGAATGAACCACTCCCTGCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCTCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587b	81	G A ---	---	---	GGCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAAGTGACTACCCTTGAAGC ACATCCCTCTG[A]ATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCTCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587a	28	C T ---	---	---	GGCTAGTGGGAAACCTCAGGTAGTCTCCGAAAGATCTGTGCTTCCAAAGTGACTACCCTTGA AGCACATCCCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCTCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-10681b	103	T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAAC ACAGAAAAGCTAAAGACATCCTTTTTTAAAAAGCC[T]A/AAAGACAGCCATTTTAACTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTTGGAGAGGAGGAGTGACGCTCTGTTAAAAG
WI-10681a	41	A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCAGAAAAGCTAAAGACATCCTTTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTTGGAGAGGAGGAGTGACGCTCTGTTAAAAG
WI-7222c	126	G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAGGCTAGGAAGGGCTGCTTGAGATGATGTTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATCCCTTGAAACAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	G A	---	---	GCCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G T	---	---	GCCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A	---	---	AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTT[C/ATTTATCTCCTCCCAAGTCAAAATG CTTGATCTTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCT TCCTGTCAACGCGCTTCCCTGGCGTACAGAGATCCTTGGCCCTT
WI-8054c	237	G T	---	---	AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTTCTTATCTCCTCCCAAGTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCTTCC TGTCATAACGCGCTTCCCTGGCGTACAGAG[G/TAATCCTTGGCCCTT
WI-8054b	148	T C	---	---	AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTTCTTATCTCCTCCCAAGTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAG[T/C]TTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCT TCCTGTCAACGCGCTTCCCTGGCGTACAGAGATCCTTGGCCCTT
WI-8054a	131	C G	---	---	AAAGATGACACTTAGAACTGGATCAGCTTGGCCCTTCTCTTCTTATCTCCTCCCAAGTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG[C/GJA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATTAGCCACTCTGCT TCCTGTCAACGCGCTTCCCTGGCGTACAGAGATCCTTGGCCCTT
WI-10854b	152	G T	---	---	TTCCACAAAACCTCCCTGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAGACGATAGTTAACGCTCGTAAAGTTTAT ACGGTGTGCGAGGCAACA[G/T]GAGAGGTACGGGAATAGTCTACTTCTCTTTTATTTTCTTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T	---	---	TTCCACAAAACCTCCCTGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAGACGATAGTTAACGCTCGTAAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTCTACTTCTCTTTTATTTTCTTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ...	---	---	AATTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTTCACGCAGTTAGCCATTGTGACAGAGGCTGTTATG/AJGCCTT CAAAGCCAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATTCAGATAATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ...	---	---	AATTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTTCACGCAGTTAGCCATTGTGACAGAGGCTGTTATG/JJGGCCTTC AAAGCCAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATTCAGATAATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G TGGGTTTT	TTGTTTGTGT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATACAAATACAGATCGIATGGGTTGTTGTGTGGGTTTTTTTTT/GJTTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8555	29	A G AG	AACTGCAAT AGGAAACCAG	CCACCTGGGGC TCCC	TTCAGTAACTGCAATAGGAAACCAGAG/AJGGGAGGCCCCAGGTGGGACAAATCATGGCTACCCG TCCCCAACAGAACAGGGGAGGAGGTGGCCCTACACCCTTTAT
WI-8170b	259	G A ...	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCTCAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAAGA
WI-8170a	204	T A ...	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCTCAAAGTGCAATCCTATCAATCAGAA A/T/AJAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAAC
WI-8172	136	C G GACA	CCTTTATTAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAAGTCATCTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACTCCCTTTTATTAAATTTGTTTCTTGACAT A/C/GJAGTACCTTTACAGGTATTACATTTCTCTTCACCCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTGTTGAAAT CAAACTGC	AGCAGGGTTTGAATTTGATCCCTTATTTACATGAAATAAAAAACAATTTCTGTGC/GJGCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTGTTTCTGTGATGAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ...	---	---	GCCTTTATGGGATTGCAAGCGTTACAAGGTTAAAGACAAAAACCCCAAGCATGGGATTTTGCCTGGAAAT ATTAGCGTTAAAGGAG/CJTTGAGTTGAGTCAAAACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGAACAGCACAGGGAGAGGTTAGTGGAG/GJGAGATGGTCAGGCTTCCTG TTCTTAACCAGCAGAGCCCGAGCAACCTAGAAAGCCCTCACCTAGCCTCTTAAT

WI-8827	22 C T	TOCCCTGGGAG ACTATGG	GCGATTAGGAT TTTAGTGTTCA C	GGTGCCCTGGGAGACTATGG[C/T]AGTGAACACTAAATCCTAATGCCATGCATTGGAAATTATT CCGACTATTACTTTCTTTAGTTCTTCTTATCCACCAGTCTTCT
WI-8833	51 A T	TCCTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACTGTCTCTTCCATGCCATTCTCTG[A/T]TGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTGCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTtagccatgttggtaaaagtTCATTTTcagTACATGGGTAACACCCAGGCCCTTCCQ[A/G]T TATATCCAGGTATGCTACAAGTTCITTTAACTCTTATCAGAAGTATTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTGTCTAATGTCCTCATTTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAAAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGGCTGGCTGTTGGCTCTGGCTTGTCTGTTTGGTTCTT TCCTCTACTGGTCTTCTTTGCTTTGGCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG AGGATA	AGTCTTCCCTGA GCCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCTCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATCTCAA
WI-8865b	52 A G	---	---	AGGTGACTGGAAATCACAGGCCACAGACTGAGGAAGACAGTATGTCGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAT[A/C]CTCCCCGTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTGTGAAATATAATAAAACTCTTTTC AAGGCTCCCATGCTTGGATGTCACA[G/C]TATGTCAAGTTAATAATAAACATTTCTAAGTGCCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCTCAGTCACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAGAAATGGTAAT[G/A]TTGTATCAGTGCATATTTCTATGAAA ATTCTATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCAGCTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAAGTTTCTTTCCATAGAAGAAATGGTAAT[G/A]TTGTATCAGTGCATATTTCTATG AAAATTCTATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCAGCTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AAGGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGG[A/G]TCCCCCTCTGCCGTTGTACCCACATCCACAGAGCA GCCCTAGTGCCAGGTGCGAGCCACTGCCACCCACGGCACACGGGAACAGGACCCATGCTGC

WI-12108	40	C T A T A	TGAAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAGGGTTAAACTCAATATC[CT]GAAATACCTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTTAA
WI-5989	29	G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA GG	CAGGCAACGTCACAAAGGTCACAGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAT CTTGTTAACTTGCCTCCATCTTTTCTTGGTGAGGACACC
WI-12201	61	C T C T C A T G	CCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCCTTTAGCCTTTTCTGGAGTGTATGTCCCAAGCCACTGATCACCTGCATG[CT]GGCCA GGTATGGTGGGGGTGATGGACGTGGTTGCAGCCCTCCACTGCTCGATAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGGAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAAGGCAGCCTCTGACTT[A/T]CTCTGTCTGTCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATAGGGGCTCTGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G C T C	TGGCTCGCTG CCTC	AGGGATCAA GAGAAAGGC	TTTTTCGTTGTTTAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTCGCTGCCTC[A/G]GCCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T T	CATGCCCTTA AGGATTAAGT	TCCTTTCTCTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTATTGATTGGTATATTCAGGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATTT GTTCTGCTCAT	GGGAAGGCTCG GTACATATTGG	TCTGATGTCATTTATTGGCACAATAATTATCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTCTGCTCATAATTT[C]CCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCAC[G/A]CTTCCAGAAATACAAAGTACTTAATACATATTTTCAAAG CTGTTTGCAATTCAAACAAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAGTACCTTTGTATAGAAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTGGGGGAGACACATTTTCCCTGGG AAAGG
WI-11321	67	A G T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAAGCAGGGAGGAAAAATCCAATAAATTTTTTAA[A/G]AAGGTTTAGTATTTCCCAATGCTATTTAATAAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGTACTGGAGCCCGG
WI-11324	40	C G T G T G C C C C A	ATCAAGCTTG TGTCGCCA	GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]AAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAATGTATCTGAAGAAGTTATCTGTCTTGTCC

WI-11352a	69	T C G	AGCAGCAGC ATAGTGGAAA	GACCTCTCGTA GGACACTTACG	TGACACATGGTTCTGTTTCCAGAAAGGAGAGAGATCATCTACATAAGCACAGCACATAGTGGAA AGT/C/GCTAAGTGTCTACGAGAGGTGAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCCATGCTGTCATTGGCAATCACTGTGAAACCTATGAAAACATACCTGCCAGGGCTCAGCTT GGAGATTCTGATTACG/C/GTGTCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAGACTTTTCATATCTGTTTAAAAAGTC TCTTCAGT/C/JAGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGAAATAGAAATCAGC
WI-11388	88	C A A	TGTTGAAAT ACACGTAAC	TGCCCTGATC CAAGTTAAAT T	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACAGTAACTAAGTTC/C/A/TATAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T G A	GGTATGIGIT CTTGAACCTTA	GTACATTCAG TGTTTGTAAA AAG	TTCTATCATCCATTAAATGGCAGGTATGTCTTGAACCTTAATAAATAC/T/G/C/T/T/T/TACA AAACACGTGAATGATCTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTGTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA TC	AAAGAATAAGATGGCATTTGTTTCAAGTTAATTTTGTGTTTGAATGGTGTGTTTAT/GATGGGTGAATA TGAAAAATAGCTTACCTCATCCCACTCTAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C	TCCCCACCA CAGC	TGCCAGGCGCT TATTTG	CTGTCACTTTCCCAACTAAACCGTGAGTTCAGATGTCTGGCAGCAGCTGTCTGTCTTGTGGTG TATTCACATTACTGAATCCCCCAACCCAGC/C/A/JCAAATAAGGCCCTGGCACAAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T	TGAGAAGCCA TTTATTTTGA	GTTTATTGTTA TAAAAATGAC CTACAACTT	ACTTTGAGAAGCCATTTATTTTGCAG/C/TCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACCTTCTATTTATCTATTTATCTCTCACATACATTT CATGTATCCTG
WI-11364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTTATTTTAGTAGAAGC/J/GJGGAACAGTTGTCAATACCTTCTGTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G AGCAGAC	GGCAGCCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATTAGGCGGGCAGCCAGGAGAGAC/J/GJACCGGCTCCTCAGTACACATT CCCCACCCCTGCCGTGCTGCCCACTCAGGCTGGGATGGAGGGGCGAGGTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTGTCATCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCA/T/J/GJGAAACATATGCAAACTAGCATCATTTGTCTCTAGA
WI-14186b	88	A G ---	---	---	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTTAGTTCAATACATG/J/TACAAATCATTAGAGTCTTTACAAGTCAATAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAGACAC	AACTAAACCA CTGTGAATTTT GTACC	AATGGTCTGGTTTTATTGAGAAGCTGTTGGTCATTTTGATGAAAGACACATAIC/TTGGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTITTTGGCTATAGTTCAGTGGTTCTAAAACCTTGAGCTTGCAGAGAACACCTTGTGGGGCTTTA/ GTTCAAAACATGGACTGATAGTCCACCCCGAGATTTCTAACTGGGTAGGCTGGGGTG
WI-12345	37 C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA/C/ATCCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCACCTTTGTGAGATTTGCAAAA
WI-13416	71 C A A A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAAGTTTTCAGAAAAAAATAAAATGACAAGAACA CATA/C/A/AAATATTGAAATTTTTCATTGAACATATAACACCTTAGCAGAGGAGGGACTTTTGTAT
WI-12310	46 G A	TTATTTCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGGTCT AAA	TTTGAAGAGATGCTGAATTTATCCCAAGTATAATTTTAAAAGCTT/G/A/JTTTAGGACCCCAACAATA TTTAAACATCTCTTACACATACAGAAATTTTCAGTTTACAAATATTCAGAAAGGCATTTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAAC TTGGATT	GGAGTCTTCGG GTCTGG	GAACCGAGGCTTTATTGGAGCAAAGAGTGTGGACACTGTTTACAACAAAACGTTCCGGGAAAACCTTG GATTT/C/TTCCAAAGCCCGAAGACTCTCCAAAGTTCTCAGTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCCTTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTAATTTGTTAAGAGTTTGCTATCTATAATTTTCATATTTATGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG/T/G/GGGGATTTGTACAGACTTTCCTC
WI-11585	79 T C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTCC	TTAGAAAGGAAAGAAATAAAACACAGGTAAATGGGAAATCAGTTTCAGAGGTAGGAAGGAGCTGGGTT TGCAAAAACAAAAT/C/GGGAAGTATCAGTGAAGCATGGCCCTAGAAAGTCCCAAGAGCAGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT/ G/C/JAGAACTAGGGACTTTTCCATGAAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTGTTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAAACAGAGAAATAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAAACCTGCA/C/ATATTAGTATTGTCAGCTAG GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAAACAGAGAAATAATCCAGAAGACTCAGCTGCTTG/G/GGG CATGTTCCCAACCCTGGACTTGCCAACTTTCACTGTGAAAACCTGCAACATAATTAAGTATTGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAA/T/C/JTACTTAATAAAGAAAATTAGCCATACCACATTTGTCCATTTGCTAC AAGAACAATTTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCCTTATT ATTAAGT	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGGTGACAGGATAATATACT CAGATAATTTTTAAAAATAAATTAGCTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTTGCTAC AAGAACAAATGGCAATGA
WI-11627	23	T C	CCITTCCTTCC ATITGTCCTC	CATTGCAACC CATCTCAAG	ACCCCTTTCCTTCCATTGTCCTC[T/C]CTTGAGATGGTTGCAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTGCGATGTCAAGTCCATCCATG
WI-11636	61	A G TCCT	GGACTTAAAA AGATCTGCTTA	AGAACTTGGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAAATGAT T	GTACCATTTCTTATGGTGGCAAAATAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C CTG	GCCAAAAGAC TATTAGCAA	GGCTCTCCCG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTTCAGCAACTG[C/G]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A A	ATTGATTTTAG AAGGAAGTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACGTCAA[G/A]CTTTACTTTGAGACAAAGCCTTGGCTGCAGTTGTTT AAATGTCCTGAAACAATCAGATTCCAGCTGGAT
WI-11680	55	T C	ACAGATACITTTCCACGCAACATTCTGAAATGAAAGCTTTGATTCTCCCTTTT[C/G]TTGCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C AGGGACAG	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACITTTGACATCTTTATCACAGCAGGGGACAGT[C/G]AAGGTTGGCTTCTCTA ATGCCACCATCTTGTTGTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T CAGCAG	GAATAATACT GAAATAACCA	AGAACAACCT AAGCAAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACITTTCAATAATTAAAAATCGAATAATACTGAAATAACCCACAG AG[C/T]TTTCAGTATAATTGCTTAAGTTGTTCTAGAAAAACACTGCTAATTTTTTTTCTGCAGA
WI-11706	60	C T TCTCTTCT	TGGCTGGAATT TCTCTTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTTCATCGCTTCTACCATCTGGCTGGAAATTTTCTCTTCTGTACAAATTTATTGCTC[η]GGCTG GAATTTGTTCTTTGGTGATTGTCCCTTGTCTGT
WI-11709	105	T A TTCAGTTTGC	AGAAGCTTGC TTCAGTTTGC	TCATTTCTCT AATTTTACGGG A	AAATATCATCACTCATATCAGGCATGTTTATAAAATGAGAGATTATGTCTTTTGGCATACTTCATC TCTTTCAGGACACAGAGAGAGCTTGTCTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A CAGTCTTCA	GCACTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACTGTCCCGAGCTTTCAGCACAAACAGCCAGCCACACTCTAGACAGCCCTTCAC TCCAGTCCATTCTGGCACTAGCCTCAGTCTTTCAG[C/A]CTCTCTCCCTCCTCCACACACTCCTTC

WI-11715b	123	C T	AGCTT	AGCTGGCTGC	TCCCATCTG TGGCT	AGAATGGAGCTGTGGGGAGGAGACATGCACACAAATGTAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGACTGGGGAAGA
WI-11715a	49	A C A A A		GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTGGGGAGGAGACATGCACACAATGTAAACAGACAAA/CJTGCATTACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTACAGCCAC AGGATGGGACTGGGGAAGA
WI-11727	43	G C T C A A C A		AACAATCCTT AAAACAAC TA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCCTATACCTAACAAATCCTTAAACAACTATCAACA/G/CJCTGCAACACAAACCACAGGC AAATGAAACAGATGCCCCAGACAGCACACCCACCACATGGCACAC
WI-11728	16	C G ---			---	TTTTATTATCAACTC/GJCAATTCATTTACAAATGTAAAGTTATCATCAGTCCCATCCACTTT CTCCCATCTTATCCTTCCCAACCCTACACTTCTCCTCCCTACAAACCGGGTCCAAA
WI-11758	61	A G T C G C T G		ATCTGTGGTTT TCGCTG	TGATTGGCCCT GTGGTCTA	TTTTCTCTTTTATTAAAGTCGCTATACCTAACTAGAGGAGAACTCTGTGGTTTCGCTG/GJTAG ACCACAGGGCCAAATCACACAGCTTCTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37	A G A T A T A A		GCCTCACAA GTATTTCTAA	AAAAGTGCTCA TCTGTGAAC TC T	CCGGCCTCACAAAGTATTTCTAAATATAATTTGCT/GJTAGAGTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAAATCACTATGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C ---			---	AGCACATGATATCTGCGTGAGTTTCTGTGAGCTCAGCAACACAGAGTCAGAGATTAAAGAATT ATTTATTGCGCTCTCTTTTTCCTCCCT/GJGTGATTGTAAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G G C A G G G A A		GGCTCAGAGA GCAAGGGAA	AAAACTCAGA CTGTAAATTTT GTTG	CATGACAACTCTTTTATTAAATGGGCTCAGAGAGCAAGGAA/CJGACACAAAAATTTACAGTCTGA GTTTTGCGGCGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G A A C C T C T G		CCCACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT/GJGCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A A G T A T A C A		TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACITT ATAAAAA	TTTTAAATCCCAAGCTTACAACCATCTTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/CJAGT GATTTCTCTCTTCTCTTTTATAAAGTGAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T A A G T T A A A		GTITTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTAAATTTTCCATTCCTCCCTTTTATAGTTTTTAAATGTGATTAGAAAAAGTTTAAATTTACAT ATGTGGCTTATATCTATTTCTA/CJTTTGACAGCACAGTCTTCAAAGTTTGTCTATAGACAATCTGA AAATGGGTCTGAAC
WI-11906	52	A G A T C T G A A		TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTAGTAGGAATGACTTTGTGTTATAACATCAAAAGAAAGAAATCTGAAT/GJTGAGGGAACTG CAGAAATTAACCTTTCAGTCTAATCTCAGAAATGCCAGAGTAAGTGAACCTTTACAG

WI-11909	78	A G	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTTG GGTGGTCAAG[A/G]CTATTTCAGAAAATCTCAGAGGAGGACAAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60	T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31	C A	---	---	CCCTAGTGAATACAAACCTTTGTCTCTGGAGAC[A/G]CCAGCTAGTCTAAGAAAACCTTCTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTCTGGGAAGAGGGAA
WI-11965	65	T G	TGAAGATCAG ATCTCTGGTTT ATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAAGTACAACACTGCTTTATTTTCTTGTCTTGAAGATCAGATCTCTGGTTTATTAA[T/ G]ATCAACATTCCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90	T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAATCACCTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[T/A]AATAAAAATACTGTAAACACATTTCTCATTTCTCTTACGA ATACTTCTTTTGTATTTGCAAAATCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95	C T	---	---	TTCTGCTGAAGATCACAACAAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTTGTACCTTT GTGTTATTTCTGTTTCAACTAAGG[A/C]TJAGACTTCAGAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTCAAAGGCCCAA
WI-15488	69	C T	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAAAACATGGTAGGGAAAAAGTTCTCACTCTGCACCTATAAAAAAGGACAGCAGATATCA AC[T/G]TTACAGAAATGAAATAGATGGAAAAATTTTAAACAAATTTG
WI-13654	49	A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTCAATGTCAGGAGAAAGGTAACCTTTTCCCAATTTTACAGACAAAAACCAGT
WI-11070b	135	C T	---	---	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA C[C/T]GTGGGGGTCTGTGACTTCCACGTCACCTGGGGATCCAAACAGAGGGAA
WI-11070a	110	G T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGGTCTGTGACTTCCACGTCACCTGGGGATCCAAACAGAGGGAA
WI-12020	121	T C	---	---	AATCTTTTATTTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATGTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTTGTTCTCCTC

WI-11076b	142 G A	---	---	CATGGTCTGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTGCAT G
WI-11076a	106 T C AGCA	AAGGGGGAGC	TCCTGCTCTGG GTATGGAC	CATGGTCTGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTCTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTGCAT G
WI-14263	49 T C GGCATATTCA	CGCAGAAAAA	GGTTATTCAAA AATTAGTAGG	ACCTTTAAAGTTTCTCCCACTCTCCGCGAGAAAAAGGCATATTCAA[CT/GTCCCATACTAAATT TTTGAATAACCTAACCTCCCTTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-14267	28 T C	---	---	AATTATTGCTGAAATTAGGAAGGGAGCA[CT/GTGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTAAAGGAAGCAAGTACCATTCTTCCAAGTATAAACTCGTA
WI-13892	50 G A TAGAAC	CTTTTCATTTT TGCTTTTAAA	TGATGATGTCA TATACTAAAA ATCAAAG	GATTGTTTTTATTCACTCTCGCTTTTCATTTTTGCTTTTTAAATAGAACAG[G/A]CTTTGATTTTTAGTA TATGACATCATCATGAATTTTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108 C G TCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT TCCCTTGG	ACCTCTTCTGATGACACTTGTACCTGTAGGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGG TACAATTACAGGATGCAGGGCATGAGAGGATTCCCTCTCTC[CT/GTCCAAAGGAAAGAGCTTTTGGC
WI-13951b	88 G C	---	---	AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAAA[CT/GAGCCCCCAGATCAGAGGAAGAG ATGGCTTCTTGTAACTTCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACITTGCTATGTGCTG G
WI-13951a	39 C T CAAAA	GGAGTGAACA AAGTAATGAA	TTCTCTGATC TGGGGTCT	AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAAA[CT/GAGCCCCCAGATCAGAGGAAGAG ATGGCTTCTTGTAACTTCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACITTGCTATGTGCTG G
WI-13264	25 G A TTGCCCAT	AAAAAGGCTC	GGAGGGAGAG ACGGGAATA	GAGACCAAAAAAGGCTCTTGCCCAT[G/A]ATTCCCGTCTCTCCCTCCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCCATGGCATGGTGATCCCTCTCTTGGGATCTGTGAATATAACCA ACTGTCTGTCAATGGC
WI-13960	39 A C TGATAGA	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C	TTATTTGTCAATTAGCAAAAGGAAGTTAAATACTGATAGA[V/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAATCTGTTCACTGTCAATTTCCCTCACAAGGAGTTGAGCCCTTAGATGAC
WI-15843	62 C T CAG	ATCTTATAACC AAGAAGCCTT	CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTAAACCAAGAGCCTTCAG[CT/GAG AGCAAGTCTGAGCCAGAGGTTTTATACACTTTGTCTCAGGGTCCACCAGGAACCCAGGCTCTGGCT

WI-13983	52	G A	TCTCTCCACT CCITTAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACTCACTGACTTAACAGAAATAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTTGT CAGGGAACATTTACAGAAATAAATAAGATGGACTTGCAGGTGTAAGAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTTCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAGAGGCCCCGAAATATAGTGAAGTCA
WI-14284	55	C T	---	---	ATTTCAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCCTTC ACCAAATCTT	ATGACCAGACCAGAGCCCCCTGTTCTATATGAAGACAAACAGGTGGCCATACCTGGGTGGAGGGATA CCGCTGCTATCCAGAT[G/C]AAGATTTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCCTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTATAGTCTAACAGGGGAACAACTCTC A
WI-13859	84	G A	---	---	TTATTTGTCAGAAITTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAGGAAACTA[T/G]AACAACAAGTATATATTCAGGAAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAAGGATACAGAAAAAACTCAGCGAAG[T/C]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCAACAGCTCCAGTTGCTCTCTCCAGTCCCATTTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A	---	---	TTTATTTGTTGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCACT[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGCCCTTGAATCTGACATTCAGATCAAGTCAG CGTAATAGAAACCAGAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTGTTGGATAAAAGGACATTTTTCATTAGCTTGTCTCAA[A/G]GAC AGAGAAATAAGATAAAATTAACCTTAAAGAAATTAATAGAAAAATTAAGGAAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTGTTGGATAAAAGG[A/G]CATTGTTTTTCATTAGCTTGTCTCAAAGAC AGAGAAATAAGATAAAATTAACCTTAAAGAAATTAATAGAAAAATTAAGGAAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTAATTAGCATGCAATGCAATTAATTCTGGCAATAAATAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[A/T]AAATGTTTCTGAATGTGCACACTAGAAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATTT GTCCCAAAAA	TCCATGTAATAATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCMAAAATTAAGATTTTTTGGGACAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAACTCTAACTGCGCAGAG AAATCAAGACCGATGGGTGAAATCTGGGCGAGCTTCAAAAATTTCTGCCTCCTAAAAACATTTTCAC CCAATTTTTCATTTATGGC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCATTTTGTGTAGCTTTTCATACAGTACAGATTTCATTTGATGTCGCTCCACATCTG
WI-15809	77 T G TGTAAATGCC	TGTTTCTGT TGTAAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCC[T/G]TTTACAAACATTGAATTAGCTACCTTAAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTCTCAAGAAGAACAGGACTTGATCAAGCTCCAGCCCTCACCACCTATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAGGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATCCAAAGATGGGAAGCGCATTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATCCAAAGATGGGAAGCG[A/G]CATTTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59 T C GCAGIGAT	GGCTGGACACT GCAGIGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGAT[T/C]JAGGG GCAGGTGTGGGCGAGGTGGGCTCTGAGCCGAGGACAAATGTCATGGCAGAGCTTCCAGAA
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACCTT/AJAGACAAAAAGATGTT CTTACACACTGAGCTTTACAGTACCCCAACATGATATTTGCTTTTCCCGAGGGCAAAAAGA GAGCTTCCCAGAAACCTC
WI-13789	62 G A AGGGAG	TTGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATTGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTGGTCTCACTCTCTT GAGTGCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGGCA GTACTTTT	AATAACAAGTTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCAAAAAAGC[G/A]TGACAAAAAAGTACTGGCGCAAGGACAAAAATAATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40	C T	---	---	GTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[C/T]GTCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAAGTAACA
WI-13367	84	G C G A	CCACTGAA GACTCACCAG	TCCCAACCCCA CCCT	GTCTCACTTTCTGTCTAGGCTGTAATTTTCAAGTTTAAACAAGTTTCTTATGTGATTGTGGCCACACT GAAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACCTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCCT
WI-13600	26	G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACITTTAATGAGCCCAAGCATCCAT[G/T]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTCTCTACCC
WI-13602	89	G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCCCC
WI-13650	76	A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTTAC TTTTAAAAAC[A/T]AAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAAGTTACCCGG
WI-14319	83	C T A	CAATCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80	A G A A A	CAATACATT GCATTTTCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTTAACTGTAATCAATACATTTGCATTTTCCCTAAAA AAAGAAGACATTT[A/G]TTCAAGAGAAAACTGGTATCATGCAAGGAAAAAGCAGAAAAAATT
WI-13909c	93	A T	---	---	ACTTAACTGGCTTATCTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G A C	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACT[C/G]AATATCTTTTTCAGAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C A	---	---	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGGACAGAAAAATTAAG AATCAAAACATCTCTGGAC[C/A]ATGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78	T C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTCAAG GTTCCCAT ---	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGGACAGAAAAATTAAG AATCAAAACATCAT[C/T]CTGGACCATGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104	G A A A	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACTT ---	AAAATTGACAAATCAACTAGCTTGTCTTTTGTCTGTTTGGAGACTACCATTTATTTCAATTTATTATGT AATACACTCATCCAGATAATGAACATCTGCGAAAA[G/A]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGGCTTTTGTG[C/G/A]TTTGGAAAGACTACCATTTATTTCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAAAGTGTGGGAATCACCTCATCTGTGTC
WI-15747	88	T C A G T G T T	TGCTTCATTT AAACTAATTT	CATAATTCCAC AAAAGTTTCA TAATTT	TGTAATCTGCTACAGTCTTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATGCTTCAT TTTAAACTAATTTAGTGTTC[C/T]TTTAAATATATGAACCTTTTGGTGAATATGAACCTGTACCAAAC C
WI-13752b	117	C T	---	---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATACTTGGCTTGCAC[C/T]GGACACCTTTTACG GAGGATTCGGGACAACT
WI-13752a	106	T C A G T G T G G A	CCTTCTCGTTA AGTGTCC	CCCTCCGTAAA AGGTGCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTCTGGATATAC[T/C]TGGCTTGCACCGACACCTTTTACG GAGGATTCGGGACAACT
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA	TCCAGATTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTACATGATTAC[T/G]CGGTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A C T G A A	TGGTGTGAAC GATAAGCACA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCACAAAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACTGAA[C/T]GCTGTGCTTATCTTTC CTGATTCT
WI-14061	68	C T	---	---	CCTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C/T]AACCAATTCATCCACCAATTTGTAAAAATCTCATCTTCTGGGCTGGATCTCAAAAAACAGAT
WI-15719	69	A C C A T T C A G C	ACCCITTCATC CAITCAGC	TGATACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACACACTACCAGCTGAATATACTGAATTAACCTATTCAACCCCTTCATCCATTGAG C[A/C]AATTTAAAACTCTTGCCAAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAAATCACACATACATAGATCAAAACAGAAGTACCACAGTATGCTTTATTTTGGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACTTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T C A C A	ATTTTATTCAC ATTAACCTTG	GTTCTTTGATA TGTTGCTTAGT TTT	GGATTTTATTCACATTAACTTGCACA[G/T]TAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72	G A	---	---	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGGAGATGTGAAGACACACAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56	A C	---	---	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG

WI-13785b	40	C G	---	---	---	TCAAAACGTCACACTATAAAAGTGCTTTAAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTGCACAAACACAGTG
WI-13785a	27	T C	GGCTT	AAAACGTCAC ACTATAAAG	TGTTGTGACAG CTATGTGTCAC T	TCAAAACGTCACACTATAAAAGTGCTTT[C/J]AAAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTGCACAAACACAGTG
WI-13793	88	C G	ATAGG	GGATTTTACAT TCAGCCTAGAT	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAAAATAAAAATAGTTTTACCCCAATTGATACAAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCCTGCCCCATAAAATCTATGACTTG
WI-13794	52	A G	TTCTTTCTC	TTGCTCACCCCT TTCTTTCTC	AGAAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAAATCCCTCAATCCATTTCTTCTCACCCCTTTTCTTCTC[C/J]TACAAGGTTAAGA GCCCATTTCTTCAACAAACAAACAAACATAGAGCAAT
WI-15729	35	A G	GTGAGACTGC	CITTTGAACCAT GTGAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/J]GAGGACATTTAGAAAAGAGCTGAGACTGAA AAGTCTGCTTGACTTCCAAAGGAAGGTAAAGTCCCTGTTTGACAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66	G A	C	TGAGGTTTTTC ACCCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCCTTTGACAAAGTCTCCCAACTGGTTTGAGGTTTCCCTCTGAGGTTTTTACCCCTATTCTTC[G/A] TTAGACCCTGGGAGAGAAAACACATGTGTAAGTGGCTCAGGACATGAGGCAGGCCGTTTACAAAGAT GCTGGCTAAGGGGCTTC
WI-14085	29	T C	AATT	TCITTAFAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATTT[C/J]GAGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAAATTTCTTGCTGCTTTTAAATCCJGAACATTCCTGAAGCAGGAA
WI-13446	22	G C	TCACATCA	GCCATGTTCTT TCACATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACATCA[C/G]CCTCTGATTTTGATCCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56	A C	TGGGTGCC	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAATGTACCTTACACATGGTGAGCACATATGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCAAAAACCTTGACCAGGCAGGTTAGAGCAAGGCATGGTTTCAGGATG
WI-15702d	107	T C	---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAA[C/J]ACTAATGGGTTCTTTGAACAAATAGTTTT TGA
WI-15702c	101	T C	---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]TGTGTAACAATACTAATGGGTTCTTTGAACAAATAGTTTT TGA
WI-15702b	90	C T	---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]TGTGTAACAATACTAATGGGTTCTTTGAACAAATAGTTTT TGA

WI-15702a	48	G C A A A G	A A C A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A G A G A C T C C G A A C A A A A T A A A G G C T T C A A A A A G [G/C] G G G G T A A A G G G G T G A G G A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113	T C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G G T A A G T T T C C T T C T C T T C T G T A G A T [G/C] G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56	G C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62	G A ---		---	T G A T T G A G C T T A G A A A G G A A G T C A T G T T G A A A T C A G A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86	A G ---		---	C A C A T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T T A A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95	A G ---		---	A G G C T G T T T T T G A G G C C T G A G G A C C C A C A C A T G A C A C G T A A C C A T G T A A C C A T G T A C C A T G T G T G A G T T A T G A G C T A G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T C A C A G C C T C T G C A
WI-14078	61	C T G C A A G A	A A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47	C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C A C T [C/T] A T T T G T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31	A G A A A A A	C A T T T A T T T G A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T A G A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G A G G G C C T T
WI-12169	121	G C T T G C T T	A A T A A A A C T T C C T A T T T C T T	G G G T T C T G A G G T G A A A G A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T C T A A A T T T T C A C C T T A T T G C T A A G T T A A A A T A A A A C T T C C T A T T T C T T T G C T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50	A G A T C	G G A G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T	T T G T T T T A T T T G G G G A G A A T G A A G G A G G A G G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T A T T T G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A T C T G C G G T T G C C A G A C A G

WI-14379	102	C T	TC TATTAACA GGGTTATGCA CACC	ATCATCTGTT TGAGGTTGACA	TTTATGCTGTTGTTTCTACTGGTGGTGGTCTCACTAATATCCAATCCTAGTATGATTTCTTT TACTTGTGCTATTAAACAGGGTTATGTACACCC/C/TGTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAAA/C/ACCCACCATTAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	---	---	ACCGCAGAGCTGCTGATTTAAAA/GIACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCAGCTGCTCTCTCCAGGACTCTCCACACCC
WI-15937	24	A G A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	TGAAACTGAAACGTTATTTCTCTCCA/C/ACACCGTAGAACTTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGAAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	AAACTGAAAC GTATTTCTCTCC	GGCCTTTAAGT TTCTACGGTG	ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC/GI/TATTTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92	A G	---	---	GACAAAGAGCGAGTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGTGGTTGACCT GCATAGATTTTGTGACGACTA/C/TGTGGCCATGCCATTCCTGTAAGTGAAATTAATGAACA
WI-14125	88	C T	GGTTTGACCTG CATAGATTTT	GGAATGGCATG GCCAC	GTTTATTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGTTCTCACCATGCTTCACAT[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14136	120	G A	ATGCTTTCACA	TCITGGGC	TTGTTGTTGGCACCAGAAAAAGCT/C/TATGTTCTATGTTATGTCACCTGTACATACTGTAACAAGACT GCATTAATATTGTTTCTTATGATTGTTTCAATG
WI-14138	23	C T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTTCAAAACTTGAAGCAACCAAGATGTCCCTTCAGTAGTATATTCA GACAAATC/G/AJAATATTACTTAGCCTAAAGAAATGAGCTATCAAGTCAAGTCAAGAAAGACATGCAGG AACCCTAAATGGATATTACT
WI-13551	74	G A	GACAATC	TAATATT	TTTTTAAAGAGTGCTTTCACATCATTTATATTGTTATGTCACACAAACTTTTTTAACTC/TGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCGAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTCCC
WI-15953b	59	C T	---	---	TTTTTAAAGAGTGCTTTCACATCAT/T/GJTATATTGTTATGTCACACAAACTTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCGAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTCCC
WI-15953a	26	T G A T	TTTAAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTG A	TTTTTAAAGAGTGCTTTCACATCAT/T/GJTATATTGTTATGTCACACAAACTTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCGAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTCCC

WI-14631	82	G A ---	---	TGAATTCAATGGACAGTTTGGCCTCTGTTTAGTGAAACCCCTCACAGCACTCTGCATAGTCGCTTT CTGCTTCTTTAAACG/AJTGCCCTGGTTCCCTCTGCCCAAACCTTTAGGATGGCCTCCTCAGGGCCTT GTCCTGA
WI-6053	24	A G ---	---	ATCACCACCGTGTCTAAGAAACAAC/AJGTCCTCATGTCCAACTCATATCCCGGGACCTTTGTCAAACCTG CAGTACACTTCTGTCATTGAACCTGGCTTCTGGAGGGAAGCCTCCTAGAGGCCAGGTAAAGGGGTGC AGCAGTGAAGGGTATATCTGGGCTGGCCAGTTGGAACCAACGGAG
WI-15964	99	T A CTGGAGGTA	GACTTCTCCAC CCTCTTGC	CAGAAACCTCTTCTGTGTAATTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTA/AJGCAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103	G A GGCAC	CCCTTCTTTC TCTTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGCAGGGGAGGC/G/AJGAAGGAAGAGAAAGAGGGGAGGAG CCT
WI-12179	96	G A TGGAGGTCA	TCGAATGACCC TGATAGTGC	TAATTTAAACACAGCCCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCTAGAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA/G/AJGCATCTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	GGAGATATTGA TCTCATTTAAA	CACAAATAGTGAAATATCTGAGCAAGAAATCATTTCTCATTTAAATTTG/C/GJAAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A ---	---	AATGTGGACTTTCAACAAGGGTTTAAACTAATCTAATAACAATCTTACAAACATTCAGAGCAT TATAACAAGAAATATTACAGGCAGCTAATGATTAAT/AJAAACCATGAAAAGAAAAAATCTG ATCTAGATGTCAGCAAAATGGGCTGAGACTGT/C/JTGCTGCTAGATGCAAGTGTGTATGTTCTAC TCTATTACAAAAATTAACAGAAATATGGCTTCGCTTGTGCAATGTTATATCACAGTC
WI-13967	103	A C AAATAAAAA	TTGTGTTTTCA TCTCCTAAAAG TG	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAAACAAGATAAAATAATGTCATTACGAGTCATTT AAAAAATAAAGACTACAGATACAGAAAGAAATAAAA/A/CJACCTTTTAGGAGATGAAAACACAAA
WI-14408	60	T A G	TTAATTGTGTA AAACTCATTTG TTACTTT	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGT/AJAAA GTAACAAATGAGTTTTACACAAATTAATAATTAACACATACTATTGGGATTTGTTGAATGA
WI-13683	47	C G ---	---	TTTTGTGTTAAGAACAGCATTTTGAATAAATAAACCTATCTGCCCATG/C/GJTTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T CGTCT	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACCTGATAAAGCAACACAACCTTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA/C/J GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---	---	ACATGGCAGATACAGAGTGTG/C/JTCTTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGTTGAAGGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59 T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCAIT/CJGTTA AAAGICAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101 A G A	CCCAGTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCCTA AAA	GTGGAATTTTATTAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACCTCAAGTCATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73 T C	GGGTTGACTT GTGGG	TCCCACTGC OCC	TGAGTTACAACAATGAGCAACAAAGTTAGAAAAATGGTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGGTCJGTACTCAATGGGGGCGAGTGTGGACGGGAGGATTGCAACACAGAGTTTCATACCTG CAA
WI-12535	50 A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTATTTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATATJ/TJCTCCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A	AAAGGCACAC GGGAA	CTCAGCCTGCC TTGACC	TTCCATTTCATTGCTTGGCTTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTGAGAAAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTCTCCAGACCTC
WI-12340	18 T C	---	---	ACACAAATATAATTCCTATTCJCGAGTGATTAACCACTTTTGTGTTTAGAACCAACAAACAACTAC AAGAAAAACATTTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52 T A	ACCCACCACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAAAACAGTTAAAAAGTACCCACACACTACCCCTGT/T/AJAAAACTTTAAG ATTGTGATGCCCTCTGCATCAATTTTGTAGAAAAACAAAGAAAAACACAACACTGAAGGGCCCCCATGTA
WI-14816	29 A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTATJ/TJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAGATC ATG/GTJTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAGATC ATJG/TJTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AAACTGAACA TTTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAG ATCAIGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T	GGATACAGCA GTAAAGATA CAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAACTGGGGATACAGCAGTAAGAATAACAAAAATCCTGC[C/T]CTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAATA

WI-14836	28 T C ---			---	TCCTTGGAGGATAGAGGACAGAGTGTTT/CJGTTGATTTTCGTTTCGGTTTCAGTTGGTTGTCATT GGTTTTGTTTTTGGCTAATTTGCCACCCTATAAAAGCAGTGCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAG GAAATACTT	TTTGTTGCTA CTTTTACAAA CITT		ACATTTCCCTTATGATAGCAACAACATAATATGATGGATGGTGACACGGAAATACTTAATAT/TTAA AGTTGTAAAAAGTAGCAAAACAAAATGAGTATATATACTATAAGTGATAGAGGATGATATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---			---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTGTG/CJAAG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACTATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTCTAAG	TGGGCTGCAG ACACTC		TTTTAATTAAACGTAAAAAGGCAGGACATTTCCAAGGCTCTCTAACA/CJGAGTGTCTGCAGCCCCA TTCGCTTTGAGATGTAATGTGTTAACCCAGGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTGAG GCCATTATT		ACGGAGTCGTCTGTGATGATTTCTTGTCAAAAATGTTTGCCTGATTCTTAATCATGAAGAACAATT AGAAAAATCCAAATTGACAGATATTCTGCA/GJAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAA
WI-14898b	79 A C ---			---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAGGTGCCACTAAGGAAA ACTTTCTCCA/CJAAGCTGCCTGCTGTGCACGTTGCCTGGGCTTGTAAACCCCTGGTGTGCTGCTCT GCCTGTGTTCTGCTT
WI-14898a	50 A C CA	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCTT AGTGGACCT		TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAAGGTGCCACTAAGG AAACCTTCTCCATAAAGCTGCCTGCTGTGCACGTTGCCTGGGCTTGTAAACCCCTGGTGTGCTGCTC TGCTGTGTTCTGCTT
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT		TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/CJAATTCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCAGACCCCATCAATCAGTACTCCTGCAGTGCAGAGGGGCCACATG CAGATGCTCAGTGIG
WI-14911	52 G A C	CCAATACATT CAGTTCTGGT	CAAAACCAGGA AAAGGACCTT		CTAGAATCTGGGAAGTCCAAGCTCAGTGCAACCAATACATTCAAGTTCCTGGT/CJAAGAGTCTTTTC CTGGTTTGCAGACAGATACCTTGTGTATCTCCTCACATGGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88 C A ---			---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGCAATTTC TAGTGATAGTAGAGGACTCA/CJA/CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCCAAAAC CTACACCTCCAACCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCAGGA CAATAAATTC		ATTTCCCTTGGTGTGCTGTAAGCCTGTGAAGTCAATGCATCTGCACACAGTTTCTCTAGCA/G CJGAATTTATTGCTCTGGCTTGTGATGGCTTTCACAGC
WI-14926	49 T C ---			---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACTTAGCGAA/CJACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTCAAAATAAAAAATTTCTTAATCAGGTCCA

WI-16083	89	C	T	ATGTTAACA CAACATATC AAGGAT	TGAAAAAGATT OCAGCC	GCATCTTTATTACCACAGAACTCATTTATGTCTTAATCATGTTTAAATATATATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAGCAG
WI-14930	55	C	T	GGAGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGTGGTGATTTGGGAGCAGAGGGAGAGCAA
WI-14946	47	T	C	---	---	TCAATACTGAAGGTGTCAAAAGTGGTCTATTTGCCCCACAGACATAACA[C/T]CTCTAAATCATCTCTA GATCAGGGGAGTCAATAAGGACCATTAAGGCTCATTACACACAGTACTTTATGGAAGGATT
WI-15987b	80	A	G	---	---	ACATTAAACACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C	T	CACAATTAAA GGGGTCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T	C	AGGAAACTG CTAACTTGCA TGA	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTATTGCCGTCTCTGAGGAAACAGGAAACTGCTAACTTGTCAAGT[C/T]CCAACA ACTGATGAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGTCTGTTCCCTCCAGCTGA
WI-16100	52	A	G	CAAAAGCTA TTTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATCTCTTATCAACTCTCTGAAAATC
WI-14958	83	A	G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTCAT TTGGGTTTTT	GTGATTGATCTGTAATATTGGGATTTATTCAACTCTAAATTCGAAGATGAAAAATTAATTTATCT CTTCTTTTCAAGGG[A/G]AAAAAACCCCAATGAATGCAATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAAATTCAGGA
WI-14976	35	C	T	GTGATTTGCT TCGTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31	G	T	TCAGTGGTGT TATTGGATTTT	CACCTCTGACA TAATACTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C	T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTTAAATCATGCTACCAGCCCATTAAGCCAAATTCAAACACCACCTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAAGCTA
WI-15002	72	T	A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACTGAAATGCTCTTCTTGA TTCC[T/A]TTCAGTTTAGGCTCAATGGGCTCTCTCCTCAAGGCTGGACCTCAAAAGGCCAGTT
WI-15000	90	G	A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGT[A/G/A]TGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68 G A	CACAATACCTT CATGTACCTAT	CACTGGACATA TTCCTACTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCAGAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91 A T	AAGGGACGAT TTAGTATCTAA	GGCATGTCCCA GTGTTTT	CATAAGTTGCAATTTATTCAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100 C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTCGCTTTATATTGGAATTTCTA[C/A]JAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38 T A CA	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA[T/A]CTCACAATACCATATACAACATACT TTCAATCACAACCTCAAAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40 A C TCTATTG	TTTACTTTGTT GTCATTTTAT	CCATAAGGCTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTGTGTCATTTTATTCTATTG[A/C]ATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTGTTAAATTTATGCAT
WI-16163	35 C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CAITTAACCTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA[C/T]ATTGTAAGTTAATGTAATTTGGCAGCAT GCCCAAGTTTAAAGAGGACTATTCTTTAAACAAAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88 T A TC	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCAATTTGAGTGTCTTTATTATATTGGGAATTCAGTGATATTAAACATTTGTACAAT GCACAAAATCTTGCTCTCTT[A/J]TGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTTGCCAT
WI-16167	58 T C GATTTT	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATAATATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C/C]ATCTT ATTCACCAGGACACACACACGACAGTAGAACAGTTCACACCTGATAAATTGCACAGATG
WI-14482	17 G A ---		---	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCTTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81 T C ---		---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCACTACTATGTGTATTCCAGTATCATGTAC GGACTAAAAAAAT[C/G]TGCTGCTGCTGCTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97 A C	TGAAGATTAA CCAGAGTCCG	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTACTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC[A/C]TCTCTTCAAAATGACACAAATTAAAGACG
WI-15012	59 G T ATGT	GCAGCAAGAT TACATCAGTA	CTCCAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATATACAGCTTTTTTTCATTGAAGCTTT[G/T]TACCT TACTACTCTAGGCTATTGGAGTGTCCCCAC

WI-15100	74	G A ---				TCTATTACAGCCAGAAATAACCAATTATTTCCAAATAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GTTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT	CCTTATTTC CCAAATATAA	GTCACCATGTT ATATTTCTTT TAAGAC		TGGTACAGAATGTTAAATTACAGCAGGGCAGTGATTCAGTTAAATAAAATTTAAACCTTTATTTT CCCAATATAAAATTACTAAATAA[A/T]GCTTTAAAGAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T C ---				TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAACACCCCAAAACCACATGGAGACAGAAG ACGAGACACAACCTCCTCCCGAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-12002b	68	G A ---				TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAACACCCCAAAACCACATGGAGACAGAAG AC[G/A]GAGACACAACCTCCTCCCGACTGCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA	TCGGAATCCA	TGGTTTTGGG TGTTTTCTT		TCTTTAATTTTATCGGAATCCAGGACACA[A/C]G/AAGAAAACACCCCAAAACCACATGGAGACAG AAGACGAGACACAACCTCCTCCCGACTGCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-15116	96	C T GTTGCAGTAA	GGGAGCCCTA GTTGCAGTAA	CCTGAATATGC AATTATTTATT ATGACA		TTTTCATTTATTTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCAATAATAAATTAATTCATATTCAGGATTTTG TGAATAGGTGATTTGGGA
WI-12578	37	C T AATGGGAA	GGCCTAAAGG	TCAAGCGACCA CCAACAC		GCAAAAGCAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTGGTGGTGGCTGTACTTGGT GCTTGTGTGCATGGAGCAGAAAGTCTTCCCTGGTCCATGCAGGGCGTCACATAATTTAACTGCACATAAT TTGGGCAAACTGTCATTG
WI-15153	40	A G GCAATTGCA	CCCTTATGTTG GCAATTGCA	AACCTCAGATA AGTGCAGTGT T		ATTTACAGTTGGCCAGATCTCCCTTATGTTGGCATTGCA[G/A]GAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTAACCTTTCTAA
WI-15215	84	G C TCAAATGGG	TGGCTTTAGAA TCAAATGGG	CCAACAGGGGA AAAAGTCA		CCTTTGTCTCTGAACCTGGGACCAGGATGTGAAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAATGGG[G/C]TGACITTTTCCCTGTGGTGGAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C T C	CTTGAGGACCT AGAAAGCAAA	TTTGATTGGCA TAATCACTCC		AGAAAGAGTGGTAAAGCAAAGCGCATCATTTGGATGGAATGATTATGTGTACAGACACTTGAGGAC CTAGAAAGCAAA[C/T]GGAGTATTATGCCAATCAAAATGCAAGGTTGGAGATATGCTAAAA
WI-15152	51	G A ---				AATTGCTAGTGCAAATGGACCCAGAAATTGGAAGGGCTATGTAACACACAC[A/G]ATATGCACACCAC AGCCATGTCAGTGCACAGATCCCTTGTGCATTCAGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55	C T TAGGATG	TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACACAGAC		TGACTGTATACCAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACACGAGATAAAACACAAT

WI-15182	49 C A	GCACAAACCAG GGCAAAATA	GCAATGGGTTAA TCCAGCA	GAGACTGCCTGTGACACAACACTAGCTAGTGCACAACACAGGGCAAAATA[C/A]TGCTGGATTAAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	GGGCOCTGGC CACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATTGGGCTTGGCACTATG[C]CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTTCAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42 T C	CATTATTGAG TATCTTGCTT TGAT	GTTGAGTCTT ACATGCTTAAG TAGAC	TCAAGTGGTAAATAGCCATTATTAGTATTTCTGCTTTGAT[C]GTCTACGTAAGCATGTAAGACT ACAACATTACGACCCATCTCTTCAAGAGGAAGCTGGTATTATGGAAAAACAATTTGTCAATTCAGAT T
WI-14510	104 A T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAAATATGCCCTACATATTTAGTGTAGTAAGTACACCCAGATATTTTTGGGAGAGAG TTGTTTGGCTTTTGTGGCAAAATATGCATAACAAAAT[A/T]TGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C	CATTGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCAATTTTGCATTAACACCATCAT[C]CCTGAG TCCACAGATAAGGTCCCGGAGAAAGGGGCTTCCCTCCTTCTCGCTGGGTGACGTTCCCGAGCGAGT GAAGCCTTTTCTGGAATG
WI-12634	52 T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATT[C]GCTATTAGCTA TGTTTACAAATTTGCTGAAAGGGTCTAGATGTGTACACCCAGAAAGTGGTATTCCTGA
WI-15249	34 T C	GGGCTTGACAC AAGATTCTAA AA	GGAAAGCCAG AGATTTTAAAC AA	TTTGTCTTGAAGGGCTTGACACAAAGTTCTAACTT[C]TGTGTTAAAACTCTGGCTTTCCCTGGCTGG TGAGGAGGCACAGGCTGGGCTTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCTCCACTCCCGAG CCACATCTTGGCTCT
WI-12159	28 C T	AAGACCCGT GCAATGTC	CCCTCTCCTCA GTGCACITT	CTGTCCGGGGAAGACACACCGTGCAATGC[C/T]AAGTGCACCTGAGGAGAGGGGGTCTGTGACTC CCAAACCCCTCGAATATTTTATGAATCTAAGATCCAGACGCGAGTTTCACACGGAGATCTGC
WI-12648	41 A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAAATGGCTAGTGGCATTAAAGGATGC[A/G]GTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTACTCCCATGTTAGGTGCTTTACTTGGATTATCTCATTAAAAACCCACA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/ T]CCATTAGGCTTTGTTGTCTCAATTTAGAGACACAGGAGGAAAAATTTAGCATAAATCTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG GA	TCCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTGATAGTGGAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGAAATTA TCCTG
WI-15325	39 T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTAATGGACTCACAGTTCCATGTGGCTGGAGGC[C/T]TCACATCATGGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC
WI-13936	123 C T	AGTTGGCATTC AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTAGTATTTTCATCCATGGCGCTTCTCAGTCCCTATACATTTCCAGGGTTGAGTAGTCTACCC CCATAGGTTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTAT[C/T]AACTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T	G	TAAAT	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTATAATATTTAACTTTTCTGGATGGTATAAATTTGJTT GAATTATAAATTTTAAATTTTATAAATAGTCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C	T	AATT	GACTTCAAAG GAAAAGAACCA	TCACGCCCCCA AGTCTTTG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/CAAAGACTTGGGGAGTGAAGGCAGAGCCCTGGTGCAGATGGACGAGGTCTGCAGA GG
WI-14546	95	C	A	GGACTCA	CCAATTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTAGAGAGACTACTTCTCTCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/CA/CTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37	G	A	TTATTGGCTGCTCTCTGTAATACAATGTGGTGAACAC/GA/CTTAAATCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGACTGCAAGACCAGTGTGAGGCACATAGGCTGATTAAATCAGTGG
WI-14580	100	G	A	GTCTTGCA	CATCCCATCT GTCTTGCA	CCGACCAAGAT CCCTOC	AGAAATTTTCTTTTTTAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTATACATATCCCATCTGTCTTGCA/GA/AGGAGGATCTTGGTGGCTTAACA
WI-8540	73	T	C	GGCTTA	GGCCTGCATTT TCAGGCAC	GCCCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCCACAGAAAAAACAACAGACTACACACAGGCCCTGCATT TGGCTTAT/CJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGATGICT
WI-8039b	97	T	C	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCAGTACGCACATCAGAGTAAATACTG TTTGGTAAACTTGTTCAGTTAAATATGTAT/CJGTGCTCGTGCATGATTAATATCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACACCACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTAATGCCGCGCCGACACCCACA
WI-8039a	87	T	C	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCAGTACGCACATCAGAGTAAATACTG TTTGGTAAACTTGTTCAGTTAAATATGTAT/CJGTGCTCGTGCATGATTAATATCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACACCACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTAATGCCGCGCCGACACCCACA
WI-8044	107	C	A	CACAACATTCAGAAGTTTCTGCAATGTGCTTCTCTGATGTCTAAAAGATTGAGCTTGGACTAT ACGATTTCCACACACTGAACGCATTCAAGTTTCTCCCA/AGATGATGGATCTCTGATGATTAATA AGCCCCGAATTCGGCTAAAGGCTTCCACACATTCAGACATTTGTAAGGTTTTCCTCCAGTGTGGAC TCTCTGGTGTGCACAAGATGGAATCGGCTGAATGCTTTCCCACT
WI-8550	32	G	A	ATGCAACAAG	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA/GA/AAATTTGTAACCTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T	A	TATTAGATAAACCCCTTTGTTCCCGATTGAGGATGTTTAAATTTGCTTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGT/AGATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTCTGTGGCTCACAACCTGCCCTGTGAGAGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG

WI-6192	91 A	GACTGCTAAG GATTTAAATTTG GAT	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATAATCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTAAATTTGGATAGTATTTAACTTAGCCATCTAACACTTCAAGCATAAAC
WI-6194	105 T A	CACATGGCAA TGATAATAAA GAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGCTCTACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACCT GTCACCAAGAAAGTACATGGCAATGATAATAAAGAAATTAATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAACAAATGGAATTTGGAAAAATAGGAGTAAA
WI-6213	164 C T	---	---	CATATGCTGCTTTATTTCTGAAGGATACACTGAACGTTAGATGATAATAGCTAATGACAGAAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCTACAAAGATGTAGTATGTATTCATTACATGTTTT ACTTTTGATATTGCTCATTTACTATATGTTCTATATAAATGTAGAAATACAGTAGGTGATCC TGCAATTCAGGTAAGCGGTAGGTGGAATCCAGATTTCTCTTGAGGAAAA
WI-6217	131 C T	---	---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAGCTCAAGGAGGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAAGTGTGCTCCAGGGCTTGACAAGCAGCTCATTCAAAG[C/T] GGCCACCATGGCCCTAGGCTGCTCAACAAGTCCAGCAGCAATCATGGCTTCGTATATCTGATCC AC
WI-6238	175 G A	---	---	ATAGCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTATGCTTTTTTTTTC TAGAAGGTATCTACATCTGCAATTTATTTACAGCCTTGTGGTATTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGAGTCCAGACTTCAGGAAATGATTT TCCACATGTTAAGGCCAGAGTCTCCAGTGTGGTCAATCCAGAACGACTTG
WI-6272	86 C T	GCAATTTATCA GGGAAAACCTT TAA	CTGTTTTTGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGTGCATAGGGGATTAGTCACGTGCACAGTCATAATAATGCATTTA TTCAGGGAAACCTTTAAATCTTTCTTCTTCTCCAAAACAGCTGCTGGAAACACCTCAAAATTA GGGATGTTCACTCTAAACACCTTTACTGAAACTTTGATTCCTTGGGCCAGAGGAGTCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGTATGCAATTCATACAGGCAAGAA TCCCAGCATCCCAGAGAAGCTCTGTCTG[C/A]CTGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGAGTTCTAGTCTCGCCTCTCGATTTCCCTGCCAGCAGTCTTCTCTCTCTCTCTCTCTCTGCCC TCTG
WI-6303	96 G A	CCCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGATGATCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGTGTGATGATCCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAAACTGGATAAAGAGTTGCTGATAGTAGT[C/T]CTGGTT CTTCCCTTTACATCTTTTGGGGGA
WI-6315b	193 C T	---	---	ATGCTTTTGATGATCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGTGTGATGATCCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAAACTGGATAAAGAGTTGCTGATAGT[C/J]AGTGTCTCGTT CTTCCCTTTACATCTTTTGGGGGA
WI-6315	187 T C	---	---	ATGCTTTTGATGATCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGTGTGATGATCCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAAACTGGATAAAGAGTTGCTGATAGT[C/J]AGTGTCTCGTT CTTCCCTTTACATCTTTTGGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGGAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAAATAAAGATCTC ACATTTGTAAGGCACATATGAACAATTTTATAGCAAGCACAAAGGGCAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TAACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ...		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ...		---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTGCAGCAGATTTTCATTATAGTTACTTAA CAGCTAAAATAAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGGAGCTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAAAC[G/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ...		---	ATTGTAATTAATAATTACATGGGCTATTATTAAGGACATGTGTAATGTTCCACTTTGTTTAAA [C/T]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAAGTTTGAAAAATGGGCG
WI-6558b	68 C T ...		---	ATTGTAATTAATAATTACATGGGCTATTATTAAGGACAT[G/C]TGTAAATGTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAAGTTTGAAAAATGGGCG
WI-6558a	42 G C ...		---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]JAGCAATGGATGCTGTGTCAGAACATACTGCCAATAAATTTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAAGATTAATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75 T C GTCATA	TCTTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTAGTTTAAATCAAAATCAATCAAACTCCAGCTGTTTCTCTTGTCTTT TTACTTAGCAAGGAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA[T/C]JACCCAACTTGAAGGTGATTGAACCCAAAAATAATGGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGTTATATTTTGATGTTGCCAAT
WI-6644	134 T C ...		---	TGCTAAACACCACCAATTATTAAGGAGAGTACTAGGAAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGACAGACTTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAAAATTAGCTGGTCTGTGTATTAACCAAGAGCGGTAICTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	TTGCAGTGTAT TAGCC	

WI-6690a	28 T C A G A G	AAACACCACC ATTATTAAGG	GCTGTGTTGG TAGTTTTCTCT	TGCTAAACACCACCATTATTAGGAGAGTTCJACTAGGAAAAAAGTACCAAAACACAGCATGTGAAAC AGTTGGGACGGTGGTAAAGGACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATAACCAAGAGAGCGGTATCTGG
WI-6770	53 A G A A C A T C A C A	CAAAACCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA[A/G]JAATTATTTCAT ACTATTATACACTCCAAAAGCAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCATTCITCCA AAAACAAAGA	CCTTGTAAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAAAGTTTCAGCAAAATCAGCTAGCACTAATCTTGACCAAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAAATTCACATTTAAACACATGGTAACTCCAAAGCATTTCT TCCAAAAACAAAGAAT[A/G]AACATTGGAAATAGTCACITACAAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG[C/A]CTTCTCTCCCTCCAGCTTTTGTGAACAAAAAC AATCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTCAGGTACAAGGTCTC
WI-6844	225 T C ---		---	TAAATAGTGCCAACTAGCATTACGTCACCTTTCATCATTAATAAAACAAAGGTAATTCCTCCTTG GTATTTTCAATGATGCATTATACAATAACGAAGTTAGAACTTAAATGACCCCTGATTAATATG TAACTGGTAATTTGTTTTTAAAGCATAATAATTTGGTTCCTTCTTCATAAAATGGAAATTTAAA TATTTCTCTGATAGTCTTGAGGTTCJATCATTAATGAGTAGTGCAAAAGTGTG
WI-6824	112 A G ---		---	CGGTTTGTACACTTAATGGGTTTTTTTTAAGGATTTTTTTCAGGCTTTGTGACGAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA[A/G]CACCTTAGAAAAATTACAT GACACGGAGAAATGCGCTCTTGCTCCTTGAAGAGCTTACAGTCTAGGATTTGACAACTCACAGT CTTAGGAAGTGGCAAGTAAGGCAAAATCTTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAGAGGCCAACATGGAAAGTGTCAAGAAAAACATTCTGATAGGTACGGACAA AAGAGTCTCTCAATCAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[T/C]JAGAATAATTAAGGCCACAAAGTGAAGTGAAGTGTGTTCTGGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCAGCTCATATTTATTGGGCACAGAGTGGGCACTCAAATATCTGATGAACCTGAACTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGGAAGAGAGAGTCCCACCATATAAAATGTATGAT CAAGTCCACAGAAAACTTGCTTCCCAAGGAATGTTTCTAATTTGGTTTCAAAAGCACACTGGTTCC CACTTTACCACCTTT[C/C]ATGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGCAGAGGCCCTGTCTATATGAAGACAAAC AGGTGGCCATACCTGGTGGAGGGATACCGCTGCTATTCCAGATG[C/J]AAGATTTTGGTGAAGGAG ACCATGACAGATGACAAACGGAAACAGTTTCTCAAAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCCCT[C/T]GGTGCATCTTAACCCCTCTCCTTTT

WI-9617	37	G T	---	---	TGCTCTTTTATTTCACGTTTCAACACACGCGGTG/JTJGGCAGAGTCTACCAAGTGCCCGCAG CGCACGCTTGGCGGGAAGTCTCATTCGTCTGTCTCTATGAGTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGCACTCTGTGGCAGAGAGGCTGAGCCCTGCCACACTGGCACCA AAGAGGTTGCACGATGCAGCTTGAGTGGGTCCAGCCGGGIGTGCTG
WI-9657	121	T G	---	---	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTCTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATCTT TGATTAATAAATGTTTATAAATGTTTATGAAGCTCATTAAGATTATCTTTTAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTATAAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	GCTGGGA	AAAAATTAAAC CAGGTGTGGTG T	CAGGCTCTGCTCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT/GC/CACACCACACTGGTTAA TTTTTTAAATTTTGTAAAGATAGGCTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAAC
WI-13119a	51	C G	---	---	CAGGCTCTGCTCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT/GC/JACAGTAGCCTCA ACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACTGGTTA ATTTTAAATTTTGTAAAGATAGGCTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAA C
WI-13112	71	C T	AGCTTTT	TTAGAAATTTT GTGTATTAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT/C/TCTTTTCCATATAATACACAAAAATTTCTAAATATCCTTAAAAAGAAAAATATAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36	C A	CTCAGTACAA	CAAAGTGTA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA/C/AJAAACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAAAAAGAAAGCCCAAGGTGAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTCCCTGTGGATGAGATGTGCACACACAAAGT AAA
WI-13020a	108	G A	CTTT	CTAATAGTGG AACCCTGAGA CTTT	TGCTATTTCATGACAGACACGTGAGACAAATATCTTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCTGAGACTTTA/G/JATCTGCAAGGGGTTTAAATAAT GCAAAATACATATATTTCCATTTTAAACCCATATTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAATGTTTTCCCAATAT
WI-12837	87	A G	AAAGTCCA	CCATATACAT ATATCAAGGT GCCATAGGAA ATGCTGTTTT	TGTATAAAAAATCCAACTGTTCCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA/G/JTACAAAAACAACAGCAATTTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCCAGGATGAGGCAGAGCA AGTTGTGCTCA

L42611b	50	G C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCGTGTCGCTCTCTCCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCAGTCTCTCTGCTATACCT GCCCATCTGAGCACCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGATTTACACCA CTGGAGCTTCACTTTGTTAC
L42611	34	T C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCGTGCTCTCTCCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCAGTCTCTCTGCTATACCT GCCCATCTGAGCACCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGATTTACACCA CTGGAGCTTCACTTTGTTAC
WI-1172b	179	C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAAACTAGGCAATTGGTTAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAG[C/TTCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A ---			TGAACGTGTGGTTAAAC[C/AT]TAGGCAATTGGTTAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A	GCAGATTGGA AGTGTAAGAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTCAG AAATGTAAGTGTGCTGCTCACTGTTCTTACCCACTTAATTTCTGCAATTTTGAAGACATGATTGAAT TCCCTTGCAAAACCCCTTGATCATGATACCCGAGTTAAACCGTTAATTAAGAGACATTAACATGG CCTGGTG
WI-1231b	141	G A ---			TCCATGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTTCTCCTTCTTCAATTAATTTCTT TCAC[G/AT]TATTCCTCACCCTGAAGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126	T C A	GGCTCTTTATT CTCCTTCTTC	CGTTCAGGGTG AGGGAATAA	TCCATGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTTCTCCTTCTTCAATTAATTTCTT CTTTCAGCTTATTCCTCACCCTGAAGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTTACA CATTCGGACC
WI-472	114	G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTCTTT TCCAGCCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATCTTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAAACAGAAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAATTTGGGCTTGAAT

WI-5791a	44 C G ---			CTATGTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTTC/GIACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCTATCTCAGTACCCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTGCCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCC/C/TTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAGAAAAAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCC/C/TTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAGAAAAAGAGAGGCAA GG
WI-5406a	42 A G ---			CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAG/G/GGCCACTCCACAGATGCAACAG GCCTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAGAAAAAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATTTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAATATTT TCAAT	CCATTCCTTCTCCCTCCCTCTCCCTTATCTCCCTGTTTCTTTTG/C/G/ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCAGGATTTGCTTCATGAATTCATCTTTCAGTTT/T/A/ATAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG...	TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG/C/T/CTTAAACCATATTTTGTGTTTA GAACTCCTGTGGCCAAACCACCTTGTGATGTGAGTGAC
WI-5481b	131 A G CTGAGTCG	TGTCATTATG CTCCAAGTAT	TTACTCCAGG CTCCAAGTAT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAGAGGAGTAGTATATGTCGAAAAATCTATTTTGTCATTTATGCTGCAGTCG/GJA ATACITGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29 G A AATTT	CCAAATTCAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTG/A/AAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTCTGTTTTCAGAGGAGTAGTATATGTCGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACITGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38 T C ---			TCATGAGTCTTCTTCAAGATGCTTGTAAAGTCCCA/T/C/CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C	---	CCCAATACITTT TTCAGGTGAA			TATTTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTCACATTTATTTTT TTTCACCTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCACTCTCCCT CCTGGTGCAATTTACTCTTTACAC
WI-5546	40	C T A		GGCACCAGCCT TTT TAGAGT	CCTGTATTTTA GCAACATGGG		CCTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[C]TACCCATGTTTCTAAATACAGG AGTAAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGGTAAATCTGATGTGGAAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T		GGCACCAGCCT TTT TAGAGT	TGCACAAATTG CCCAGG		TGTTGTCTGCACCTCCCAACAAGTGTCAATGAGCCTCAAGGGTTTGTATGAGCGGGTATGGGT GGGCTATCGGCACCAAGCCTTTTAGAGT[C]TCCCTGGGCAATTTGTGCAC.TAGTGTGAGA TAAGTTGATTTAAACACCTCTGTGCCTCAATTTTCTACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGGTGGATAGACATGAATACTCTGATGACTGGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]TCCATTTTGAATTTAAGCTTTTGAATTTGTTTCCA ATG
WI-5836b	161	C T	---		---	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGGGTTCAACCCTCGATGATGGGCGTTCAAGGAGGTGGGA[C]T]GACAC ATTACTCTCCAAGTTCATCAGAACACTTCAACAGCG
WI-5573	58	C T		GTTCATAAGG AGGTGGGA			CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCAGGCTTCCCTCTATGCACGGGTCTATCTCTATATGGGCAATATCCAATGTCCCATTC[G/A TTTTTGCCATTTCCCTGTATATCAAAACAGAGAGAGGGTGG
WI-5850b	134	G A	---			---	CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCAGGCTTCCCTCTATGCA[C]TGGCTCTATCTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCCTGTATATCAAAACAGAGAGAGGGTGG
WI-5850a	92	C T	---			---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACATCACAAATATCTTATTTCTGCCTG TCACACTAAATTTGCAAGCATTCAAATTGATTGACTATTATGAGCATCGTGTCAATTC[A]T]CAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612b	125	A T		CTATTAATGA GCATCGTGTCA TTC	TTCTCTTGAGA AACCTAAAC ACTG		TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACATTCACAAATATCTTATTTCTGC CTGTCACACTAATTTGCAAGCATTCAAATTGATTGACTATTATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612a	44	T A	---			---	
WI-5636	26	A C		GCCAAATTTAT CCGCAATAAA	CATCGAGGACT TTGGGA		TGAGAGCCAAATTTATCCGCAATAAA[C]TTCCTCCAAAGTCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGCAAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ...	---	TTAGAAACCTCCATTTATTCTGCGATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCATTG ACTGACTCACTCACTTGCTCTATCAAAAATTAAGC/GIAAATAATTAATATTTTATTTACAGAGGAA CTCAGAGGCCAGAAAAATGACCAAGACACAGTCCAGTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAAGACAGACAACTAAATAATCCAGG
WI-5865b	99 T A ...	---	TTAGAAACCTCCATTTATTCTGCGATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCATTG ACTGACTCACTCACTTGCTCTATCAAAAATTTAAACAAAATTAATATTTTATTTACAGAGGAA CTCAGAGGCCAGAAAAATGACCAAGACACAGTCCAGTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAAGACAGACAACTAAATAATCCAGG
WI-5865	165 T A ...	---	TTAGAAACCTCCATTTATTCTGCGATGGTACATCTTTTAAAGAACTTTTTTTCATTATGCATTG ACTGACTCACTCACTTGCTCTATCAAAAATTAACAAAATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGTAAJCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTC AGAGAAGACAGACAACTAAATAATCCAGG
WI-5874	76 T G	CATAGCATGG ATAATATTAT ACAGAAAA	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTTTTCATAGCATGGATAATATACAGAA AAAAATTT/GTACATATCAAAATGACTGAACCTTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGAGCCGACGTTTCAGCTCTCAGTTTTTCCATC/AJTTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTTATTTCAACTCTCATTTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTG AGAAAAATAGTAAATG
WI-5752	36 A T	CAGCCTCTCAG TTTTCCATC	TTAGCAGAAACAACAAAAATGTCACACACCTGCAGTAAAGAAAGTGTTCCTCCGATAAATA/C/GJC CAATTAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGGAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAAA CATTTGTTGAAACGGAAGCCACGTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760b	61 C G ...	---	TTAGCAGAAACAACAAAAATGTCACACACCTGCAGTAAAGAAAGTGTTCCTCCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGGAAGCCGAGTTTTCGATTACACACAGTT GTCGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG/GA/TCCACGAA ACATTGTTGAAACGGAAGCCACGTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760	187 G A ...	---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG/GTTCAGAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGTGTAAGACTACTCATTTCTCAGTCTTCCCTTGCTG
WI-5944	52 A G	TTCTACCATG GGAATCTTG	GAGTTTAATGAATCTGTTCCCTCTCTAAACCTCTGTTCCCTCACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTTGCCCAAGTCATGAGGAGATGCATGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGTAC/TJTTGCTCTGTGCGGTATCTGCTCCAATCACCATTCCACATTTATTTCTTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148 C T ...	---	

WI-5967	165	CT	---				GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTATTTTGCCTAAGTCATGAGGAGATGCATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGTGACTTGTCTGTGCGGTATTC/TGTCTCAATCACCCATTCACATTTATTTCTCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53	GC	---				GGGTAAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCGAAGTTCGAAGTTCGAGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACATTTTCAGCAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	TC	AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG		GACTCTGCTCAAGAAAAAATAATGAAAAATGAATAATTAAGCACCTTCTTAATAAGCAT CTACAAGGTACTTATTC/CACCTGTTCTGGGGTTTCAATCCTCTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAAAATTTGCTCTTT CTC
WI-6450	45	TG	GTGACA	CCAATGACTT ATTCTATATCT	TTGTTTGAAT GTGTGGTACTT CT		ATAGGACAGTTTTCCTCCAATGACTTATCTATATCTGTGCACAT/GJAGAAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGATTATTTTCACGGTCATGGTAATATGCATGTAAAGACTA TTTTACTGGCTCTCTTTATGCTATAAAACAAGGTATTTGGTCTATTCAACAAACATGTGCAATACAG CAGTTGTCATGCCCTCTGGTACTAGAAATATAGTCTTTATAGAATATGTGGTTTAGAATAAAGCCACA AATTATCTATAAAACAACAC/C/TJAGGGAACGAGGCTCAAAAGTGGAAACAAAACGGCCTTAGTTTC TAAGTGAAGACTAAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-7466c	141	GA	TTGTCTCTGG	TTTTACAGTC	AGTCGCATGCC AATTTATAATT		GAACTATCCTTTAGTGGTCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT/CJATTTCAGTGAAGTATGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT CTGGTGGGAATATCTCACAAAATTAATTATAAATGGCATGGGACTTTCTGATTAGCCTGACAGGA TTGTCTCTTT
WI-7466b	80	TC	GTC	GACTTCTGGG CTATGAAATA	ATACTAGTTC ACTGAA		TGCTTTTAAAAATAACAATGACCACACCTGACACCATAGTCTGTCTCCATTTGCCACGCTTCCTC AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT/CJATTCTCTCAGAGAGACACTTGGCCCT CATAGGCATCCATAGATAATTTGTGAATGAATGTGCTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104	CA	---				CCTCTAACAGAAAACTTGACTTCCTCAACTCAAAATACCCCTTCTCTAATAATTTJ/GJAGTAACCA AAATATCTCTCAAAATAAATACTTTTAAATTAGAAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9720b	55	AG	---				

WI-9720a	47	A G	---			CCTCTAACAAGAAACCTGACCTTCCTCAACTCAAATACCCCTCTCTA/GIATAATTTAAGTAACCA AAATATTCCTTCAATAAATAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123	A T	---			CACGCTCTAAGGCAGGATGGCTTATGAGATACCTTTGCGATGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACCTCTCTGTCATGTCAGATGAGAGGCTCAGGGTGTCTATGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTAGTTGCATT TAAGAAATGCCAGTCTTTTGTCTGTCATCTTGAACATTAATCCACATG
WI-9748	74	C G	---			CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTCTAAATTTTATATGTTTACCCCTTT GTCATTTC/GTTCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCTGGAATCTTTTCAGAAT TACAGTTATGATGCTCTTTTATATCCCA
WI-9943	91	T C	---			TGAGGCTATGATTCAGATTTGTAGTGACTAATACCTTATTAAAGCAATTTCAATGTGTGGGCACTGTT CGTTGTGTTTATATCCATCTCT/CJATTTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAAATATTGCATTTTCACACCTTCTCTTTTGTCTATTAGGGA
WI-9891	39	T C	---			AGGGCTTTCACAGATCCGTCAGCTCAACACTGCCCTCTT/CJAGTGAGCCTGTGAACCAACCAAGAC GGCTGGTCATCAGTGTCTCTCTCTTTCCGGACAACCTATCTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCAATAATCTTGTGTTAAATCTCTTATTAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCATCTACACAAAAAGGGATTGCAAA
WI-9897b	84	C T	---			CTCAGAAATTTCAGATCTTCCCAATGTATGATTCCTGTTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/CJ/CAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A T	---			CTCAGAAATTTCAGATCTTCCCAATGTATGATTCCTGTTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/CJ/CAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115	C A	---			AGATAACCTGGAAACTAGAAGAAATTAATAACGTGTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACA/CJ/AGCCCAAGAAAAAGCC TGATATTAGAGGCACCTTGCAATAA
WI-9935a	42	C T	---			AGATAACCTGGAAACTAGAAGAAATTAATAACGTGTGGA/CJ/TACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACACAGCCCAAGAAAAAGCC TGATATTAGAGGCACCTTGCAATAA
WI-9983	146	C T	---			CCTGTTAGGTGCCAGAGTCCATGCTCTTGCCACAATGTTAGGCTGCCTCCCATTTCTCTTTGA TTCCCAAAACCCCAAGTTCTACCCAATCTGATCAATGCTGACTAGGTGCTGCTGCTGAGGGTAA AGCATTATGA/CJ/TAGACACAAAAAGAGAGGTAAAGTTGCTGCTCCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T A T C T	TGATGTAATGC TATGTAGCAA	TGATTACTGT GCTTAGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTTGTATTATGCTGCTATAAAATCAATGGTTCTTA ACATTCAAATAGATCTTTTGGTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTA/TTCCCTTAAGCACAGTAATCAAGGCTTCTACCCCA
WI-10020b	122	T A T T T	GCGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCTCATCTTGACTCGTATTAAATAAAATTTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAAATTAAACAGTCTAGGGTTCGGAAAGTGCGCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A T A A A T T	TGTCATCTTGA CTCGTATTAA	AAATCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCTCATCTTGACTCGTATTAAATAAAATTA/TC/TTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAAATTAAACAGTCTAGGGTTCGGAAAGTGCGCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10064b	170	C T T T A C A T G	CCTTTAGATAT ATTGTGATTGT	ACCCTTCTGAA GCCAGATTTC	TCTGAGTCTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAAATTTGCAGAGCACTCTCTCCTATGCACCAGATATTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATGTC/TTGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C A C A G G G A A G G	GTAGCAGGAT	GAGATGCTCTG CAAAATTATATT TATTAT	TCTGAGTCTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGC/TA/ATTATAATA AATATAATTTGCAGAGCATCTCTCCTATGCACCAGATATTGGTGACACTCTGTTTAAATCCAGTA TCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T C C A A A C T C T T	TCTCTGTCCC CAAACCTCTT	ATTCITGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTGTCCTCCCAAACTCTTA/TC/TTAAATTCCAATCAACAAGAAATTTATAGAA TATGCACCACATGCCCAAAAGACACCTTATATTAGT
WI-1319	40	A T A T C T T T	TGGCACCCTAG AACATAGTTT	GCCACACACC CTATGGT	AAGAAAATCCTTGTGGCACCTTAGAACATAGTTTATTCCTTTAT/ACCATAGGGGTGTGTGGCTTATCT TTTACCTGGCATGGCTTTAGGTCCTGTTTATAAATTTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGCTTATGATCTCTATTTTAAACATTAACACTGGTCAGATGTGTTTAAAACTTGTTGAACCTGCAGC
WI-10316	104	T C C T C T T	CTGTTGAAATG CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACTTAGTGAGGTGTAATCAGAAGCATCTATATTATTCACCAGTCACCAACCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTCTTA/TC/TTAAACTTTTGGATACATTCCTCAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCCCAGCC
WI-2572	61	C T T	AGTGAGTTGTGCACAAATTTGGAGACATCTGTGACCCCAACTTAAACACTCTCTCCACAC/CTAC AAAGTTAACACTTACAGTTACCAGGTGATGATTGAGCAGA

WI-10368	31 C T	TGAAGCAACC T AGGCTTGTT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAGGCTTGTTGTCGTACCCCTCTTGAAGATAAATATAATATCTT GAGATAGGAGGAGCAGCCTGAGGACAGCTGGGTTTGTCTACCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAACTATATGACCTTGATGGATTGCCTTTCAGGG T
WI-10391	32 A G	CTGCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGCTCAGGTATGACTCCCAAGTCAACTCTTGACTCCTAATCCCATCTCGGTG TCTGCTTCCAGGGACGATCTGACACAGCCTTTGCTTGCTGTGACAAACAGAACATTCGAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA GCAA	TCGCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTCTTTTTCATATT TTCCAATTTATTAATACTAGAAATTTTACCACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTT CTAATAGCAAACGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	GGGTGCTCAAT AAATATTATT CTTT	...	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTCTTTTTCATATT TTCCAATTTATTAATACTAGAAATTTTACCACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	GGGTGCTCAAT AAATATTATT CTTT	AAAATCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTCTTTTTCATATT ATTTTCCAATTTAATACTAGAAATTTTACCACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	CAAACCTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGCTTT C	CGTTGGGAATATTTCTATCTCACCTAAATATGTCGCTGATTAAATATACATTTTAAACAACTCAAA TTGCTTTAAGTACTTTA/C/GJGAAGACCTTGACTGTTGGATTTTGAATTTTCTTTTCTTTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	GGGAATATTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATATGTCGCTGATTAAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGAATTTTCTTTTCTTTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTCCCTCAAAACCCAGCTTAAATCACAATCATTCTTTCTCCTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAGAATGATCCTATTCJACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTACCAAGTGAATTATGACCAAAATGAGA/C/TJAAAT TTGTTAAAAAAAACCTCAAAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTGT ACCTACAAAATAGGATAGTCATGGTTGGCAGACTTTCTTTCTCTTTCTTTTGT/GJCTCTTA GAATCCATTTTGTCTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGGCTACTATTACCCCATGGGGTCAT AGAGAGGATTAACACAGGGTGATGCCTGCAATGGGAATATTGAAAACC
WI-10656	59 T G	---	---	---

WI-11169b	154 T G T T T T	TTAACCAAGA G T T T T T C A T T C	CTAACTTAAA A T C C T C A T T C A A A A T A T A A	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAAATTAAGCCTAAAGTAGTGCTTTTAAACCAAGAGTTTTCATCTCTTTT TTTAAAAAAGAGCAGACAGT/GJTATCATGTGTTCTGATAAATTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G T T G A A A A A	AATAAGTGAA A G T A A C T G A C T T G A A A A A	AACTCTTGGT T A A A A A G C A C T A C T T	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAAATTAAGCCT/GJAGTAGTGCTTTTAAACCAAGAGTTTTCATCTCT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G	CAAGTGCTGGACCTGGATAGGTG/GJACCGGCTGAAGTTGGACAGTTGTTGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTCTCTTTGGGTTTACCACAGGTTTTCATCTT AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATCCAAAAATAGCCATGGGTTTGGACAAAATAC AAGTTAGTGCTCTCTAATTTAATGGGCATA
WI-10686	133 C T A A G G	TGCCCTGTCC T A A G G	CAATCTCTAAA T T C A T G T G T A G A C A C A	AATAACCTGTGGCACAATAAGGCAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAAACAAGATGATAGTTCTGCTAGAAATCTTGAATCTGATGCCCCGTGCCAAGG C/TTGTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGGG
WI-11175	77 T A A	AAATGATTCTT T C T G C T C A A A G	CTGTTCTACA T T C T T T T T G A A A A	GGTAGGATGATCTAGAAATGCCACTTTACAGCCACTGAAATATATGCTCCCAATGATCTTCTG CTCAAAGAGT/AJTTTTTTAAAGTTATCTACTTATTTATCTGCTTTTCAAAGAAATGTGAGA ACAGTACAAAATGTGTTCTAGTATAGCAAAATTAATTAATAAGTAAAGAAAAAGGCCAATT TGGGC
WI-10694	144 A G T A T A G T T T C	TGCAAAATGCTT T A T A G T T T C	GGCATTTTGTA A A G G A G G A A	TAGAGAGGCTTTTCTAGTTTTCAGGTTGGAGGGGTGGTGAGGTGAGATTCCTTTAGAGCAGTGGC TATGTACAGAAAGATAAATCTGAGAAAGAACTCAGTTCTAAAGTTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTCCTCTTTTACAAAAATGCCATCAATCCCTCAAGGAAAAAAGGCTTTCT T
WI-2716	23 T C C	TGAATTCATCC A G A A A A A C A G	TCCTTTTCTC T C T T G T G T C A T T C	GTGAATTCATCCAGAAAAACAGC/T/CJGAATGACAACAAGAGAGAAAAAGAGATAAAGGTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCAGTGCATGGAGCAGTG
WI-10719	115 T C G C C A T T C T A G	TGACTCTCAAG G C C A T T C T A G	GOACTGCCAGC A G C C	CAGGCCAACTCTGTGCAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCATAACTAA
WI-10721	40 A G C T T G C C A	TGGCTCTGCTA C T T G C C A	GAAACTCCAC A T A A A T A A A T C T C A	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCTCTTCCCTGCTTAGGTTTGAAGAAGTTGAA

WI-11204b	88 T C ---			GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTACACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTTCACCT	GCTGTGCTTC CATAACAGAA	AAGAACAAATG CATAACAGAA CCTTAA	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11206	127 A T ACTC	GGTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTGG	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11215	68 C T ---			GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTCTACACT TTCT	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11219a	18 G A ---			GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC
WI-11222b	136 G A GGCTGG	CATACCACTGC	CCTGGTAGCCA AGTTGTGA	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAAAATTTTAAATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAAATAGCTGAGGAAAAATTTATTCAGAAG GCAACATC

WI-1122a	25 C T A	GCCACAGTGG AATCATTTAC	TTTATGCCATA TTAATTCATTA	TTTATGCCATA TTAATTCATTA	TTTATGCCATA TTAATTCATTA	AGCCACAGTGGGAATCATTTACACTA/C/TJGAAATCAGCAAAATGCTAAATTTGGGCTTTGGATTTT TGTTTTGTTTTTTCATAGACCCACCGTTGAACATATTGTTAAACATTTACCAGCATACCACCTGCGG CTGGTGCACAACCTGGCTACCGAGGAGAACCTGACAGACATTCGTAATTCGTTTCACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTATGCCATA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTGCAAGTTTGTGTTTATGCCATATTAAATTCATTACACTC/TJACATCATATTCTTAGCAAAATACA TCTAGACACCTGGCAGCTCAGTAAGGATATTCGGACAGATAATCATTTGTTATCATTTAGACATTTGCA GGAACCATATGGATGGATAAATGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165 A C ---	TTATGCCATA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTAATTCATTA TTAATTCATTA	TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/CJGACATAGTTGCTAAGGATATTCACACAAATTA TTCATGA
WI-10778	62 A G	GCAAGGGAGG AACATTTACA	TTGATGGGAGG AACATTTACA	TTGATGGGAGG AACATTTACA	TTGATGGGAGG AACATTTACA	CAGTGGCTGGCTACTGACAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/GJG TCCATCTCTGATGTACACAGCAGGGCCAGGAAGGGTTGATCTGGAG
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	GGGACACACT GCTCTAGACC	GGGACACACT GCTCTAGACC	GGGACACACT GCTCTAGACC	TGGGACACACTGCTCTAGACC/C/TJCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACGCAGAGGCATCAGGGCCTAGTCTCTCTGGGACAGTGAAGGGCCACACC
WI-10810	58 C T GCAGGAATT	CACTTTCATGG GCAGGAATT	CACTTTCATGG GCAGGAATT	CACTTTCATGG GCAGGAATT	CACTTTCATGG GCAGGAATT	ACAGAAAAATGCCTAGTCTGTAGCAAGAGAGGAAGCATCTTCATGGCAGGAATT/C/TJCATTT CTGTGTTTCTTAGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
WI-10828	23 T C ---	CACTTTCATGG GCAGGAATT	CACTTTCATGG GCAGGAATT	CACTTTCATGG GCAGGAATT	CACTTTCATGG GCAGGAATT	GGACCAACAGAAATTACTTGGCA/TJGAGGGTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAATACAGTTAGGGAACATGTGGATGAATTTCTTTAGTAGAG GACTTCTAAAGGCTAATAATTTGGATACATTAGGCTCATTTATGAATCTCAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CATTAATCTGC AGGCTCTCC	TATGCCTTCCCAACGAGCATCCACGCTGCTTAGCACAAAAAATAGAAATACATCATTTCTGAATG GGCACATTAACTGAGGCTCTCCG/CJTTCAGTCACCTGCAGTTAGGTAGGTGCGAGACACTGTGA TACCATAAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTCCGG
WI-10834	96 C T GTGTTAAT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	GATTTGAGTATTATCAAAATGCCCAAAGACCATTAACAAAGATTAAATAGTTAAAGCCAAAACATATA AAGAAATTAACGTTCAAAAGTGTGTTAA/TJCTTAATACCAATTTTATAGGCCACCATTAACTT CTGAAGAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24 T C ---	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	AGAAATTAAC GTTCAAAAGT	GGATGATGTTCTGTGGTCCCTTAA/TJCAAAGGCTCTTGCAATCCCCAAATGTGTAAATTTATTTATCT TGGTATTTCTCGTTACCCATAGTCACCTGTCAAGTGTTCACCCCT

WI-2296	81 A	GA	TGTTACTTTGA TTCTTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTTAGAAATAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTTGCAGAAAGTTACATTTGTTTGTTG
WI-2300	77 G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTCGAAATTTCCCTTTATTTGAGCGGGCAGGTGGTAGGCACAGAAAGC CAGTCATAC[G/T]GCTTTAAATTTGACCCCAACCATTAAGAAATAGCATTTCA
WI-2371	55 G	T	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGAAAGGCTGGTCTTGTTCTTCCCAGCTTCT[G/η]GTGGTGGCT GTCAATCTTTGACATTCCTTGCTTGACGCTGTATAATTCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCGTGCTGCTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAAGATAACATAGATAATCATAAATACCTTGGTTTAC TGAAATCTGAAACCTTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCGAA[A/C]CTGAAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTTAAAGAAAGCTAAATTTAGTAAACAATCTTTA CATTTACACAAAACCCA
WI-2437c	192 G	A	---	---	CACAGCCACCACCTACAACTCCTCTGTTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	A	---	---	CACAGCCACCACCTACAACTCCTCTGTTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	A	---	---	CACCAGCCACCACCTACAACTCCTCTGTTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	A	GCAACCTACT GACAAATTTAA TTTATGTT	AACAAGTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTT[G/G/A]GTGAGACCAATAGCAGAGTTGTACCTGCAGAAT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAAC GTACCAAAACAT G	CTGTAACCTACACACATCCTCCTGTAACTCTAGTGTACTTTGTAATACAAAACACAATGTAAATGCT ACATAAATAATGTCATACATAATTTTAGGAAATATGACAAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCCAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTATCCACAG AAACCAACGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGACCGGTTGCAGAGTCTGGGGGAGAGAA[C/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTTGTCAGAAAGAACAGAGGAGCGTT

WI-2906b	77 T A	---	---	CCTGAACACCTGGAGACATTCCTCCCTTGGACACCTTCATTCCTGCTGGACATTCCTGCTGGAACTTTGCTGGAATGCTC TTTCCCTCTAAGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTACGCTTCAAAGTGACCT CCTTAGAGTTGGTTGCTGACCAACAA
WI-2906a	50 A C	GACACCTTCAT TCTTCTCTGG	AGAGCATTCOA GGCAAAAGT	CCTGAACACCTGGAGACATTCCTCCCTTGGACACCTTCATTCCTGCTGGACATTCCTGCTGGAACT GCTCTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTACGCTTCAAAGTGACCT CCTTAGAGTTGGTTGCTGACCAACAA
WI-1736	175 C T	---	---	TACTCCTCATTCCTCATGTCCCTAGACGTAAGTCCATGCTGCTGAAACATTTATTCCTAAAT TAGATTTCCACCCCGAGCACTATTACACAGAAACAGCATGGAGCAGTTGGAGCTGGCTCTTAGA GAACCTTACTTAAGGACAGTGGTTTCCATCTGCTCTCCA/C/JAGAGATCTAGGGTGTCTTTGGAACC ACCTTGG
WI-1851	136 G A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAACTCTGGGGAGG ACACAAACATTTAGACCATAGCAATTGAATTAACATAGATGTGTTAAGTAATTATTAACATGGTA CA[G/A]ACAACCTCAGTTTAACATTGCTAGTGTCCATGTGGATACCATGTACCTTCTTACATCATG TGA
WI-3000	62 G A	CCCAAAACAC AGAGACCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGCTTACATCTCTAAATGTACACCCCAAAACACAGAGACCCCT[G/A]T GAGTCTTAGTCAATCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177 G A	TTTTCTCCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCTCTGG	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACT TAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTT TTCTCTTTCTGTTTGTCTTCTCCCTTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATTCGAGCTTTCTGT AGCCACAAGATT
WI-3167	37 T A	AAATTCACCC ACAGATCTAT TAGATTCTC	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAAATTCACCCACAGATCTATTAGATTC[G/A]CACCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140 G A	GTGGAGTGGGC AGATAAAGA	TCACTCAAACCT AGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCAACTTGCGCAGCAGAGAGGGAAG AAGTTCAGACCCGTTGGGTAGGATAAGTGATCCAAACCCCTTGTAGGGCAGGTGGGAGTGGGCAG ATAAAGA[G/A]CCAAGCCCTAGTTTGAAGTGACACTGTGGGGATTCAAG
WI-1775	47 C T	CCTGCATGGTC TTTTCTCTG	AGTTGAGATT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTTGTGAGCCAAACCCCTGCATGGTCTTTCTCTG[C/T]TTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A	AGCATATTCA TTGATTTCCTT ACAT	GAGGACTTAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATGATTTCCTTACAT[G/A]CAAATGCTC CTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCATTGAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCTCAAGTTGTAGCATTTCAGAAAGTC[CTCTCTTAGAGGTAGTTGTGCTCGTCTGTTAAAA TATGTTTCAAGATAGTATCTCCCTGTTGTACATCTCTCCAAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGTACCTCTGACGACACAAATAATTAATCCCATTCCTTAAAGACACAGG
WI-3453	70 C T	TTCTTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAAACACAGAAATTAACAAATGAAAAATCAGCTACTCTCTTAGGCCCATCAGAG AAT[CTGAAGTCATGGGAAAAATGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCACAGTATTTAATGAGGTGGT[GA]TGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCAC[AG]TATTTAATGAGGTGGTGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGGTTTCT GGATGCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCATAAAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCT[CT]TGGAGGACAGGGTCAACCCAC
WI-3600b	146 G C	GGTTTCTAAC TGGATATAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTCTCTGACTCTGCTGCTTCCAGAGTCTGATTCATGCCCTG ATAGTTCTGT[GT]GAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG TAAACATCT[GT]ATGGAAGGCTGCACCTGGATGAGGTCAACAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTCTCTGACTCTGCTGCTTCCAGAGTCTGATTCATGCCCTG ATAGTTCTGT[GT]GAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCAACAA
WI-3678	125 G T	---	---	TAAATCATGCTTATTTTCAAGAGTATCCACTCACATAGGCAATGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCT[GT]CTCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAAATTTACCTTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTAATCACTGAATGAGTTCCAAAAGCCTTTATGCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACTTCCATGAAAAGTAAAAACACACACAAAAATGACATAAAAA T[AC]JAAAACTACTATAGTTTATGAAAATGACTTCCAAAATCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCATCCAGAACTACTCTCTGCTTCTTAACTTGTGACTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA AAAC	GGTCAACCAAT CATGTTTTT	TCTAAATGTGAAACCAAGAAATCTGTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT[CT]ACACCCGGTTCAATGAAAAAACAAATGATGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGCAATTAAGT

WI-1819	51	C T	---				GAAAAAGCAGGAGCCAGGAGGACAAACATTTTGA AAAAGTCTTTTCAGCAC[C/T]TCGTGGATCCG AATTTAGTGTGATTTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTCAGTGTTCACAGAAATTCG CAGATTAGCGATTGTTGACTTGTCCAATTAATGAAATGTGGA AAAAAAAGGGTGGTAACCTGTT AAGCCTGCTGCAATGTTAGACACAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	---				GGCCTATTACATGACACTGGGCCAAGATCTTGCTCCCTTTCTTCAATAGATAGACTAAGTAAAGAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTG[C/G]AGCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	CAA	ACAGTCATTT AGTCTTCTG A	TAAGATAACC ATACTAGGTAC ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTG TTTAGAAGCA	TCGTGGTGTG CTCTCC		CAATGACCAATGTCTTTAGAGCAG[A/C]GGAGAGGACACCGACGAGACACACAGGAGGAGTGAG GTGAAGATGAAGCAGTGTGACGAGCCACAAAGGTGAGGAGGAGCAAGGGTGTGCGCCACT
WI-3901	114	A G	---				GGACCAATTGCCCTCAGAAGTACATTCAAGCCCTGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCCTCACCTGACAAAGTG[A/G]TATCATGTGTACACTGC AGTGTATTATAATGCTGCAT
WI-3914	99	C T	GC	TGATTCTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACCTGAGGAAACATTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTTCATTGCTTCTAGACCTATAACTAG ACTCAAGTCCCGACGAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTGTTCTGTTATTGCTGTTTACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTATAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T	GTCAATGCA TG	TTGAGGTCTTA GTCATTGCA TG	TGAGTTCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTGTTTGTGCAATTTATGCTTCTCTTATGTAACACAATCACCACACATTGAGG TCTTAGTCAATGCA TG[A/T]TGATAACAATATTTGTCACCTAATAGGAACTCAAGCATAGTTATGTT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC		TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGAGGTTAGGTTGGCTTCAAGATGGTAATT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAATTTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGGTGGTCTAGCAATTTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCA ATCATGATG	ATGCCTGCGATATACITTTCCAAATGACTAGTAGTATGAATAAGCACGTAATAAATTTACCTATTATATTT AT/CJCATCATGATTTGCTGCCCTCTTTCCAAATTTACTACAAATGTATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCCACTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCGTG[C]/TGGTCTGTCTCTGTTCTCTTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
WI-4250b	117 A G	TAAGTGCAITTAAGTACAAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACACAGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAC AGG	CTTTTACAGGA TCCITCCCAC	TAAGTGCAITTAAGTACAAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACACAGG[G]/TGGGAAGGATCCTGTAAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCCAT CACCT	GGCTACTTCA AGTTGTGTAAG G	TAAATGTCTGGGGAGATAATAGGAAAGGTCCCATCCCTCTGATACCTTGGTGTCCGCCCATCACCT [G/C]CTTACACAACTTGAAGTAGGCCCATCAAAACACTGGTCAGAAAGATATACTGTGCGAC
WI-4256	57 C T	ACAGCCTCTTCAATGGCACAAATCAAAAGCACCAAGTAAAGCAGAGGCAAAATCTGG[C]/TCTCAC CATTGGAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAATGATTGGCCTT
WI-4325b	71 C T	AGTTCACCTGCCTAGATGAGTAGACCATTGTTGCTTTGTTAAATGTACATGGGCAGGACCGGAAATGG GATG[C]/TJACTATAGATAATCTTTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	AGTTCACCTGCCTAGATGAGTAGACCATTGTTGCTTTGTTAAATGTACATGGGCAGGAC[C]/TGGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4347	158 A G	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGGTAACTTGGATGCCACTTCTGCCCTGTACCTTCT CTAGACTCTTGACCCCTGAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCACCTCCAGCCAG GGCCCTGTATCTGTTACGGCC[C]/G]GAATCGTCAGGCTCACAACCTGTTGGAGGTAGGAATGACGA G
WI-1936	117 T C	CCAGTCTAGGCTGCAAGGACTTCAATCTGGGCAAGTCCTGGTGTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACCCAGGGGACTTGTATCACCT[C]/CTCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCTTACTTCCACTTGAAGAAAGGAGGGGAAAGAGA AAAGAGGACTTTGACACACAACCTTGGGA

WI-5204	54 C T	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTGGGTTTTGAAGAA[C/][G]GAAGAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCACAGTTTGACTGGA ATATAGAGTGATGTCAGGGTGG
WI-5215	70 A G C T C A A A A A			AGATAATTTTG TAAAGATAGTT TTGGC	TTTTCCCTTATTTATTTAGGAAGCAAAJGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[G/][G]CGGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGCCCAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G A T A T A A			AATTAAGAA ATCTTTACATG GTTCTTT	CCCTGAAATGTGCTTTGCTTCCTCCAACTCTCTAGGGAACCTTTTCCATGTGAGGTGAAGGTTTTGA AGAGTACTTTTAATTAACCTGTATCAAGAGATGGGTATATAAT[G/][G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTCATCAGGGCTCTCCACTGCTATCAGTAA
WI-4456	49 C T T A T A G T T C C			AGTTGAATTA TTCAGAAAT GCATGAACCTTG	ACACATTTCTATTTGCTTTAAGTTGAATTTTCAGAAAATTATAGTTCC[C/][T]CAAGTTTCATGCATAA CAGGAAACACCAAGTTGGGCAATTGATTGAATTGT
WI-4461	49 A G C C T T C C			TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTAAAATTATCCTTCC[A/][G]TGAAATTTGGTGAAAA GGTCAAGAAATGAATTCCTACCTTTTAGAATTTCTGGAAATTTATTTGCGATGATAATGCAATGGGC CTACTGGATTTTACTTTTGTCTCAAGCCAGACACAGAAAGTATATAAGAAAAACAGTTAGTAATCTT TCACCTTTT[G/][A]TATTTCTCTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T			GGTGAAGATT ACTAAGTGT TCCTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[G/][G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C			TGAGAGGTGGG GACAAAA	GGGGTTAGGACCTCGAGATCTTTAGAAAGCACAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATC[T/][C]TGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T C T G A T			CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTAGAAAGCACAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/][G]CAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G			TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCCTCTGCAACACTCCAAGTAAGTCTATCATCTGAGATG[T/][C/] GAGTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCATCCAGGCTAGGGTCAATGGCATCCATGGTGGCTGGACAAAGATGGGCCCTAGGATCATTTT

WI-4540	110	A G	GCACCATGTGG CATCC	GACAAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAATTTGGTGCCATAGTACTGGCTCTGTGTGTCATCAGGAAGCAAGCCCTAT TGCTCGGTAAACAGTACTTTTGCATTAAGCACCATGTGGCATCCAGTGGCATGGCTGCAATGGCTGCTCCAGTG AAATGAGACAACATTCCTAT
WI-4582	226	T C	---	---	AGCAAGCATCTGGCAAGCCTGGGTACCAGAACATTAAATTCACCAACACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAGGCCAGTTTAACTTATCCTGTACACA AATAACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGC AAAATATGGTT/CJCCCTCCTGTAGAAACCAATTGAT
WI-1965	105	G C	AG AG	GCAATGTAGG AAGTGTTAA	CAAAAGTTAGTTAACTTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG/GCJAGAGAGATGACCCATCCATTCCTTGG GCTTCTTATATGACACCATACTATTCACACAGATGGGAGTCATTTAATTTGGTTGGTATGACAGT CATGG
WI-5248b	99	C T	TTG	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAAAACCATAACAGTTTGCTGTCTACGTTGTAGAGCAACCCAGAAAAATTTAAACGCGCTAC CATTTTCACTGTTTTCTATTGACCGTACTTG/CJCTTTTGGCTTTTTTCCCTTCCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38	G C	CTACGTTGTT	TTTTAATTTTC TGGGGTTGCT	TGTTTAAAAACCATAACAGTTTGCTGTCTACGTTGTAGAGCAACCCAGAAAAATTTAAACGCGC TACCAATTTTCACTGTTTTCTATTGACCGTACTTGCTTTGCTTTTTTCCCTTCCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69	T A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCGGTGACATTACTCTGTTGACTTTGCTCTGAAGCAGAAAAGCACTGTGA C/T/AJCATTAATTAGGCCCATCTCCTGCCTGAAGCCTGCCTACAGCAATTTGTAACATATGGCATTTGGG ACATATCTCTGAGCCCATCAACTATTGTGACAAGATTCTCCTTTTTTAAACAA
WI-5252	119	A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAAGAGCTTTGGGAAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGTTT/AJCTACCATGTACA TATTATATGAATTAAACAATGTAAAAATAGTATGACTAAGAAAATATTGGGCCCT
WI-4606	61	A G	CT	TAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAAGGAAAAATGATAACCCAGGACTGTTGTTCAAGCAATGCTAGAAAAATATGCCTA/AJ/CJ CAAGTAGACAACATTAAGCACCTTAAGGCAGAAATGAAAATTTCTCTCTGTCATTAAAGTCTCTATTCA ATTACCATTTATCGGGTAAATTAACACACTGGAAGTAATGCCAGGCTAATTTGTTAGATTATGATAAT TACACGCTTTTGCTATGCT
WI-5257	77	C A	GCAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGCGGGCAAAATTAAGCATATGAAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAAGAGG/CJCTTTTCATCTGCCCTGGTGGTTTTTCAGTAACCTGCAACATGCTTTGGCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCACCTCCTAGGTATGCACCCATAAACATGGGTG GCAAAAT
WI-4649	50	C T	TTCCGAATG	TACTACAAAGA AATCATC	TCACGTGTTAGAAAATTTCTTCTCCTCAGTGAGACCATTCTTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTTAGTACATCTATGAGCACACAAATTAACAAGTACTTGTACCTGAAATTTGATTTTTTTAA AAAACTCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGATTTGTTGTTGTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCTAGAACGACAAAGAAAGTATAAGTTGTCCTC TTATATTGCTTTTJ/A/G]CCAAATCCAGTTTAAACATTCAGTAACGTT
WI-4677	82	T	C	AAA TCCAAAAGTG ATTAGGTGAA CJT	TTTCAACAGTG TCATTATTCAA CJT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGCCAAAAAGTATTAGGTGAAAAAT GAGTTGAAATAAATGTC/JAAGTTGAAATAATGACACTGTTGAAAAATGATGAATCTGCTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGTCATCATGAGGAATTCGTAGAAAAATTTTACCTGGCAATTGATTCAAAAATAAGTTTGTC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTTGACGGAAGAAAACTTCAA C/G]TTCGAGAAGGCTTAGATTATATCGCTGAAGGCCATTCTG
WI-4722	88	G	A	AACACCACAC TGCACTATGG G	AATATGGAATC TGCACTCAGTT G	CTTCCCATCTGCCAGTTAGATGACTGCCTCCACAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCATATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACITTTGATGGTTGAGATTTTCAAGAAACGTGAAATTTAGTAAACCATGGG TCAACTATGATC/A]CCAAACACAGCAGTGTGCTCTAAAAAATATGATAGTTTCTCTCTGTCACCC GCAATGAAAAGGAGTT
WI-2028	176	T	C	CCTGTCTCATC TGTTACGTTT G	GGTTGGAACT CAAAATTACCTA GAA	GACTACAGGCGCAGACAGAGGCAATGTGTGGCTTGCACAGGTTTGGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGCTCATCT/C]TTCAGGTAATTTGAGTTTCCAAACC TGTTGG
WI-2033	183	T	C	A GGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAAGTTATACAGGACCATGTTGGAAATTT AGCATTTCTGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCAT/C]GGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCTCCTTCCACCATCTCCATCTTCTACTCTGAT/C] AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T	C	CCAAGGAC CCACAGTGCA CC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTTCTCAGAGTCCCTGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGCGTTTCAAGTGAAGACGATGAACCTCTCATCTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGACT/C]GGACCTGCACCTCTATCTTTACCCGTTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTTAAA GTGTGTAAGT ATTAATTAG	ATTCCTCTTG AAAGAAACAT CA	TCAGGTGACAAAGAAAAGTCACATTCTTCAATCACTCACCATTGTCTGTTATTGTCTCTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAACCTGTGCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTTTATGATA[C]/TJGATGTTCTTCAAGAGGAAAATTTGTGTAAAGAGGATTCCCATTT TGCAATTCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTCTCTCAGTCTTTATGCTTATTTCTTGGAAAAAAGTAGGCTAGGAGAA CACAAATTCAGGTTCTCTCCAGATCGAAGAGATAACTAGAAAATGC[C]/TJGAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATCAGTGCATAGAATCATCTTGCTAAGTTCC[A/G] JTGAAAAAAAATATGCCAAAAATTTAAATTTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACITTCATTC	CTACTCTTCT ATTCATAATC CAAAAA	CTTACTTCCAAAGTGTTTCCCGAGAGACCACCTTCATT[C]/CJTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGGCCA
WI-4818b	121	G T	TGATAATGGG GCCCTGTT	CCITCCITTTA TATGTATGCCA GA	TATAATGTTTGTCCATAGTGGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATTCAGAAAGGAAAATATACATATGGGTGATAATGGGCCCTGTT[G]/TJCTCTGGCATA CATATAAAGGAAAGGCTAA
WI-4818a	43	A G C	TGCCATAGAC TAGGTTATGTC C	CATATGTATAT TTTCTCTCTG AATAAAT	TATAATGTTTGTCCATAGTGGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTAT ATAATAATTTATTCAGAAAGGAAAATATACATATGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAGGAAAGGCTAA
WI-5317	139	T C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGTTGATCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATACAAATTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATAT[C]/GGACTCATTTCTTTTGCATCTATTTCTAGGTTATTTGCAGCCCGGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATCCACTA CCTCATTTAT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAAATCGGAGTAGTGCCTT
WI-5328	44	A G	---	---	AACATTTTAAACCATGCTACATTTACAAACACTGAAAAGACAG[A/G]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGAG
WI-4897	93	A G	---	---	GCCTTTTGTAGTTAAGTCTTTTGTGAGTGTCTTTTTTTTCCCCCACTAGGTAAGTCTCGGCCCAAT CCCCAAAAGAAAATAAGCGCTTG[A/G]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTGAGTTTAAAAATCCCTG/AJCCCTGCTATGTTTGTGTTGAAGCCACATCCACT GAGGTATATTCGTGCTGCTATTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGACAG

WI-5370	143 T C	AATAAGATGG TACCTTAACCTA CAGAGAAATTC	CAAAGTTGGTA CAGAGAAATTC AAA	TGCATGTTACTCTCTGGAAATCATAAAGGGATCTGAGAGCCCTACAGTATATGGCAACATTAAACCAAT CTTTTGGAAAATTTACCTGTATCCCATCATGGTTCAATTTGCAAAAAATAAGATGGTACCTTAACCTA ATAAAACAATTCCTTGGAAATTCCTGTACCAACCTTGGCTTTTC
WI-9711b	423 T A		---	GATCTCCTTCATCCCTCTCCAGAGAGGAGAGAGGAAACACAGAGAAACGCGCTGGTGACAGGCC CCAAATTCCTACTTCTATGGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTGGCTGTGGAAATATTTCCCTGATACCTTTAAATTTGAATG
WI-9711a	390 C A		---	GATCTCCTTCATCCCTCTCCAGAGAGGAGAGAGGAAACACAGAGAAACGCGCTGGTGACAGGCC CCAAATTCCTACTTCTATGGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTGGCTGTGGAAATATTTCCCTGATACCTTTAAATTTGAATG
WI-9702c	345 G A		---	GGAGGAATTCAGGGTGAATGGAGTGTCCCGCTCCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTTAATGATCTCTGTGACTT TTTACTAGCTTTAAGAGGTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344 C T		---	GGAGGAATTCAGGGTGAATGGAGTGTCCCGCTCCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTTAATGATCTCTGTGACTT TTTACTAGCTTTAAGAGGTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702a	179 C T		---	GGAGGAATTCAGGGTGAATGGAGTGTCCCGCTCCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTTAATGATCTCTGTGGA CTTTTACTAGCTTTAAGAGGTTTCATCCAGTGTGCTACAGCATCTG
TIGR- A003N21	49 C A		---	TATAGTATTTACGAAGCCTAGAAAGCAGGCTGTGGGTTGGTTCAGTATCTAGGT ATATAATACTTTGAAGCCATAACTTTAACTGGAGTGGTTGATTTCTTTTTTAAATTTATTTGGGA GGGTTTGGATTTTAACTTTTAAATGTTGTTAAATTAAGTTTTTGTAAAGGAAACCATCTCTG TGATTACCTCTCAATCTATTTGT
TIGR- A004V30	203 C T		---	AGAAATGGCTACTTCATAGGGCAGAGCAGCCACTTTTGGCTAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAGAAATAGAGAACATTAACAAAAATAAATATGTTCTATTTGGGAATACCTAATATCAG ATACTAACAAAGTACAGTGATAAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G,TCTCTAGGTTAGTAGAAAAAGTT

TIGR- A004W22	232 C A ---			GGATAATCAGTAGACAATAATGGGACCTTAAACTGCTGTGATGCAGGAGTGGAGGGCTGGCGAGTG CCGAGGCAAGGGAGGAGAGTGGGACAAGGGATGCTCAGTGGTGGAGCCACAGCCTGGGCTCTGGGA TGGGCATGGGAATGACCAGGTTCCACATCATGCACAGCAGGGGCTGTAGCTTGAGTTCAGACAGACAG GCCTGCCACATGGTGTGCTGCCCGGCTA(C/A)CTGGAGATGTCTCTAAAA
TIGR- A005D24	138 C T ---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTTGAAAATTCCTTTGAGATAATTGATTTCATATTTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATCCAACTCTTTATAGAGAAATAAAAACCCAAATTT CTC/TJTTTACCATTAGTTGATTATCATCTGGATTTCACCTCAAGATGCAGCTCTAAGATTATT GTTATGTTAAATTCATAAATCTTCACCTTTAATAATTAAAGGAAACAAT
TIGR- A005D24	123 A G ---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTTGAAAATTCCTTTGAGATAATTGATTTCATATTTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATCCAACTCTTTATAGAGAAATJN/GJAAAACCCAA TTTCTCTTCCACATTAGTTGATTATCATCTGGATTTCACCTCAAGATGCAGCTCTAAGATTATTTC TTATGTTAAATTCATAAATCTTCACCTTTAATAATTAAAGGAAACAAT
				TGAGTCTGAGCACGAGTTGCAGCCAGGCGCAGTGGGAGGGGTCTGGCCAGTGCACCTTCGGGGGC GCATCC(C/G)TTAGTTTCCACTGCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTTCTGTTGGATGACTTTGAGATTATTCTTTGTTCTCTGTTGGA GTGTTCAAAATGTTCCCTTTAA
U03735	74 C G ---			GGTTTGCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAAT/CJCAACAGCAAAACAAAAACCA CAAAACAAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTCACTTTTTCATGTCACAAAC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGTTATTCAAAAATTCATTGTGATATTACTACAAA GACGGCCCCAAACCAATTTTTTTC
U39840b	42 T C ---			GGTTTGCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAATCAACAGCAAAACAACJACCCACA CAAAACAAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTCATTTTTCATGTCACAAAC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGTTATTCAAAAATTCATTGTGATATTACTACAAA GACGGCCCCAAACCAATTTTTTTC
U39840	56 A C ---			GTGGCCATGATCTGGACCGTCCCTGCCCCACTGTCTGCCGJGJTAGGACTGGGTACAAACATCCA AAAGTTCAACAACACAGCAACTGTGTGCTCATGGT
WI-8997	41 G A OCCC			TATACACTTCCAATTGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTGAGAA AGCACCCAGTTTCATGATAGGAGTTTCAGGTGATATGGTACATGTTGACCTGATGACCCAGAGTCAAAATTCAG TTTCCACCAAGCCAGTAAACAGGCCAAGAGCTGTCTCTCAAAGJGJGAGAGTAGTTATCTGACAGA AGATGGCAGGGCTTGCTCCGAAAGCCTAGAGAGCGCCACTGTGATTACCT
WI-7008	180 A G ---			GGTCCCCACGAATTTGCTGGGAAATCTC/TGJTTTTTCTTCTTAAGACTTTTGGGACATGTTTGACTCC CGAACATCACCGACGGCTCTCCGTGTTTTCTGGGTGG
WI-9005	26 C T TGGGAATCT			TCCCAAAAGTC TTAAGAAGAA AAA

WI-7593	46 G A ---	---	---	TTTTGTTGCTCTGGACACCCCACTGCTCCAGGATGAAAGGAGAGG/AJAATGAGATCAGTTTTGGGACCTTCTTGAATATAAAGATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCCAA
WI-6962	78 A G ---	---	---	AGTGCATCTTGGGGAAAGGCTCCAGTGTTATCTGGACAGTTCCTTCAITTCAGGTGGGACTCTTGATCCAGAGA/GJGACAAAAGCTCCTCAGTGAGCTGGTGATATCAAGACAGAGAACCCCAAGTCTCCAGTCCCTGCTATGCCCCCTATCTATCATAGATAACATTCTCCACAGCCTCACTTCAITTCACACTATTCTCTGAAAATATTCCTTGAGAGAACAGAGATTTAGATAAGA
WI-7059	43 C G ---	AAGGCACCA GCCATC	GCTCTCGCTG GGTCA	GCAGAAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC/GJTGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGTGAAATATACCAAATCTGCATCTCCAGAGGAAAAATAGAAATAAAGATGTTGCCAACTCTTAAAAAA
WI-9063	53 A C TT	CACITCACTGA AAGACACCAT	TCTACTTTCTG CCCTTGGGT	AGCAGCCATCACATGATCTGTTTTCACCACCTTCACTGAAAGACACCACTTTATAC/ACCACCAAGGCGAGAAAGTAGAACITTAATTCATTAAATGTTTGACACAATTGGAAATGTG
WI-7079	293 T G ---	---	---	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCAACATACCATCTGTAGAGTTGGAACCTGCATTCTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTCTCTATTTCTTTCCATTGCTTATCTTGAGCACAAAATGATAATCAATTTATACATTACACCTTTTGTACTTTTCCAAAGCCC
WI-7104	38 A G AAAAG	GGTAAAAGTT CTTTTGTCTCT	GACAGATTTT GACCTAGTTCC	TTTACAGCTTGGCACTTTCTCTGCCTAGGCTGTAGGTAACCTGGGAT
WI-7104b	249 C T ---	---	---	TGGATGCGGAGGTAAAAGTTCTTTTGTCTCTAAAAGAA/GJAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTATATTTTAAGGATGTTGCCACTGGCAATGTAACTGT
WI-7104	157 C A ---	---	---	GGAGTTGCCCTTCTTAAGGGAAGGAGATCTTTATCTTCTGGTGGCTTGACCACTACGTTGGGAAGAGAGAGAGTGCCAGGAGACCTTGAGGGCAGCCGGTCTCTACTTTGGACTGAGAGAAGGAGGCC
WI-8974	34 C T AAGAACTCA	CCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA CCTGGC	CCAGGCTGGAGCAGCATGAGGCCAGCAAGAAAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTAGGCCCTTGACCAAGGTGGGGGCCACAGCACCAAGCAGCATCTTTGCT
WI-9161	61 C T CCTGGC	CCTAAGCATTG CCTGGC	AGACTAGACA GGAA	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA/CTGCCAGCTCAGCCCTACACCAGTTTCCACC
WI-9014c	93 T C ---	---	---	TGGAGTTTCATGCAAGGGCAAAAGGCAAGTGGCCATGCAAGCTGTTAA
WI-9014c	93 T C ---	---	---	CTGTAGGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATGGCCTGGC/CTTTCCTGTAGTCTCTCTGTAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCAAGTCACTTTCTCTGTTCCAGAGAGGTGGGCTGGAT
WI-9014c	93 T C ---	---	---	GCTCCATCTCTGCTCAACTTAT/CTGCTGCACTGAGCTGCAACTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTCCCTCCCCAGTCATCTTTC/TTGTTCCAGAGAGGTGGGGCTG GATGCTCCCATCTGCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGCTACGGGTCCCC TCCTTTTGGCCCAAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATCAACAC A/C/AJACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/CJCCCTGCGT GCTCAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGCTACGGGT CCCTCTTTTGGCCCAAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGGACCCCTTGGCCCTTCCCT/CJGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCAAAAGTTGTGAAGCAGAGAGAAAGCTGGAGGAGGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTATTATTGTGGCCGTGTGTGTGTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAAGCTAAGCCAGGAATAAAAGAAAGTAGAGATAATAATCA[G/A] TTCCTTACAACCGATGTAATTAAGCTTGATTCACAAGACTTCAIGC
WI-9174	47 T C T	CTAGACCCC ATTCTCTATT ACTG	TCTAGAGGTA TATAGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTAT/CJGAGTCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAITGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA A	CAGAGGTCTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAGAAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCACCTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A CGCA	CCACTTCTCCC CGCA	AAAGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGCA[G/A]ACCTAGGTGACACTTCCCTTCACTT
WI-9193	94 G A CA	AGAAATTTGT CTGCCTTAAAG CA	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAAATTTTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGTCTGCCTTAAAGCA[G/A]TACCCCTTACACACACACCCCTGTCTCTC
WI-9015	48 C T ---	---	---	TTTGGATTGATATCGTGAATCTCCAGCCGAGAAATGGGCTGGATTG/CJGCTTTGGTTAATACAT CTTTCCTTAAAGAGATAAACACAAAATCCATCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGGACAC[GJGTCCTTAATGACACCCACTCTTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAGGAAGGGAGGAGCCACTCTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G C	CAGGTCOCOA GATTGA	CAC TTGCCAC ACTCAGAC	GTGACCCGTGAGGTGAGTCCCGCAGATTGAGCTGTGAGTGGGCAAGTGTCTCAAAAGGGGGC TGCCCCCGAGGAGATGAGGTGAGAGCAGGGAGTTGAGGCCGGAAGTCA
WI-7836	120 T C C	CAAATAAACA ATGCAACGTTG	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGATTGAGATAACACTCTCATTGAGTAGTTACTGAAAGAAAACCTGCTGTA GAATGATAAATGTCATGGTGGTCTATAACTCCAAATAACAATGCAACGTTCCCTGATTCGATTTCTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCCATACCAGCT
WI-7286	65 T C A	CAGCTCAGCT TAACTGACAG	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTTCAGCTTAACGTGACAGATTTC TGTTAAAGCTTTCTGGTTAGATTGTTTTCATTTGGTGATCATGCTCTTTTCCATGTGTACCTGTGTAATATT TTTCCATCATCTCAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTTT	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAAAATGTTAAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGACGTGAATTTTAAATTTGTTATAGATGTAAACTTTTAAATAAAATTTGGGGTGTGG
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA	---	GAAGATTAAAGGAGGGTGTGCTGTGGTCTCCTCCCTGCCCTCTCCCCA/CIA/GTGGGGAGAGACCC TGATATTGCCAAGTCCCTGGACCCTGGACCAGCTACTGGGCCCTATGGTTGGGGTGGTGGCAGG TGAGCGTAAGTGGGGAGGAAATGGGTAAAGTCTACTCCAAACCTAGGTCTCTATGTGCAGACCAG ACCTAGGTGCTCTCTAGGAGGGAACAGGGAGACCTGGGGTCCCTGTGGAT
WI-9064	29 A G TTC	CGTACCTCCAA ACATAATTGA	GCTTGAGTGA AGTCTGCAGA	CAAGCGTACCTCCAAACATAATTGATTCTGATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGGCTGGCTACTGTCTCTGCACTGTGCTTGTG
WI-7307	128 G T	---	---	CACACTGTCTGTTCTCAGTGTGAGGTCTGCGAGGTGAGGTGGGGTAAAGCCGGGTTCCACA GGCCACAGCCCTGGCAGGGTCTGGCCCCCAGGTAGCGGAGAGAGTCCCTCCCTCAG/GTAACT GGAGAGGGGACTCCAGGAATGGGAAATGTGACACCACCATCTGAAAGCCAGCTTGCAOCTCCAGT TTGCACAGGGAATTTGCTCGGGCTGAGGGCCCTGTCCCAACCCCGCC
WI-9274	25 C T G	GAAATGTGAC TTCACITTTGGT	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTTGGTGCTCAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA GTTTGGAAATGCACITTAATAGCTGGTTTTTACACCTTGAITTCGAGGTGGAAA
WI-7313e	266 T C	---	---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGTGTGATTAAAGTCTTAAAT TGTTTTGCAGCTTTTATGTTTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGGTATCCACCAGTTTTTGTATGTTTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGAATAATCGTTTTTAACTGAATAGAATTGTATAGCGATGA
WI-7313c	256 C T	---	---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGTGTGATTAAAGTCTTAAAT TGTTTTGCAGCTTTTATGTTTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGGTATCCACCAGTTTTTGTATGTTTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGAATAATCGTTTTTAACTGAATAGAATTGTATAGCGATGA

WI-9281	68 G A ---	GC TAACAC TTT	---	ACTGGTGGGAGACTGTGAGGATCCAGGATTTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG IG/ATGTTAGTTTGAGTCTGTCGCTCCCTCTCTATGACTGTGCCC
WI-7848	142 A G CTC	TTAAACCGT GACA	CATTTATTTG AAAGCTATTCA	TTCTGAAATATACCAGCCATTGAGCTATTAAAACCTGTAAATTTTAAATTTACAAAATATAA AATAGAAGACATAAACCCAGTGGCATCTCGTGACATAAACAATTAATGCTAACACTTTTAAAA ACCGTCTCAGTGTCTGAATAGCTTCAAAATAAATGTGAAATGGT
WI-9304	70 G A ACTGA	GTATATTACA ATGATCACCG	CCGACAGAAC TATTGTAAAC	TCACGTTGGTGGTCTCTCAGATTCTGAGGAAATGCTTTGATTTATTAATGATCACCGACT GA/G/AJAATATTGTTTACAATAGTTCTGTTGGGCTGTTTTTGT
WI-7933b	314 C A ---		---	TTACAGAACTTGCCTGTGCTGCCCATGCTAGGGGGGAGGGTCTTTCCCTCTCTTCC TACCTACCCCTTTCTCTGGCCAGGGCTGATCTACCTTCCCTGCCCCCTGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTGCACAA AGTCAAGGGACCATGGCTGCCTGCCCTTGGGAGGAACCATAGCTCCCT
WI-7933	96 G C ---		---	TTACAGAACTTGCCTGTGCTGCCCATGCTAGGGGGGAGGGTCTTTCCCTCTCTTCC TACCTACCCCTTTCTCTGGCCAGGGCTGCTGATCTACCTTCCCTGCCCCCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTTCAGAGCTGGCCCTCGATGCCAAATAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCCTTGGGAGGAACCATAGCT
WI-7374	182 T A ---		---	CCAGATGTGCCCATCAGTTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAAATGAAAGAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGAAGAATATATTGTA/CAGAAACACAAAGGCTT GAT
WI-9343	78 C T CCTGTGCA	CCAACAACAT CCTGTGCA	AAATGAAACTT ACGTTTGTG	GGTCTGCTCTGCTACCTTGACCCCTCCCTTCCCTGCTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA/C/TACACAACAACAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104 T A ---		---	CTATATGTGAGAGGGGTGATCTGGATGGAAAGTGGGCTGGATGATCTCCAAAGTCTTCAACTCT TAAAGACATCTTAATCCTGAAATGTAACAATTTGTTA/TAGTGTTTAGAAATCAGAAATTTGATTTTGA ACTTGAGTAAATTCATCCTT
WI-9357	75 A G ---		---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTCACTTTTGTTATTAT GCTCTTA/GTGAATTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79 T C TTGG	CTTTAGAAAA TCTGCTTTAAC	CCTAGGGAACA CAATTAGAGGA	TGAAGGGGTGTGGCACTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAAATCTG CTTTAACTTGGT/C/ATCTCTAATTTGTTCCCTAGGAAATGACGTGCCCCAAG
WI-7423	107 T C GTTC	TTGCTGGGCTGT	GGTCCAGAAGA GCGCG	TGCTCCCTGTCCCATCTGAGTGACCCAGGACCCCCCTTTGAGGAGTGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTCCT/CJGGGGCTCTCTGACCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTGGGCTCTGGGAGGGTGGGTGAATAAAGGCATCTGCT

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA A AAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGAGGGGAAGAGAGAGATTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAACATCGCCAACTAGAAACGTTTCATTCTGTCATCCAAAGAGAGAGAGGAAAGAAAAA TTA/JACAACTTCATCTCTCTTCGACGTTCAATAACATTCTACATA
X86400	118 A C			TCCTGCAAGAAGTTCTCAAGCCCTTTTGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAATTTTAAAGTGAGAJC/JCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAAATCTAAATTAATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA
WI-8053	242 T A			GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAGAGTGTCCCATTAAGAGGACTTTTAAATCAACCTAA TAAACTCTAATTCGCTGACTTTTAAAGATCTAAGGTCTTTTAAATACATGCTGAAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAAT/JA/JTTCAGAAC
WI-6190	165 G A			TACACAAATGAATTGCTTTTATTCGGTATGCATCCACATTTTCAGCATTTAGTGGTCTCTGAACAGCAAG TGGAAGAGCGCAGCAATTTGCCAGGAGGTCAAGCCCACTTTCGGGATCTGCTGTGCACACCGG GTTCTCTTAATCCCTGCTGAGGATCTTG/JA/JAAGCAGCAGCAGCAACCAAAAGGCATGCA CGGATTCAAGGTTCTTTTGTCCAGTTGTAGATTCCAACTAGACCCCA
WI-6275	148 G C			AACAGTCACCACCAACCATGACAACTCGCCAGGCAAGGCTTGTCTCCCTCCCTTGTGGTCCC ATGTGCTTAGTCAGCAAGTTCGGGAGGACCGGATGTAGCTTCGCCCAAGGAGTATTACAGAGA GAGGCTTGGGAAAG/JC/JGGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCAGTAACTGGTATGCTGAA
WI-6421	41 G T			ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATGTG/JG/GGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGACGAGCAGGACCGTACCTGAGAGGGGATGGGGCTCTCTCAAAAA GAATATTTGGGCGAGAACCTTGAACTGGCCACAGGAGACATCCAAATATCCCTCTCTCTCAGGG CTCACCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A			GGTGAGACGGGTTTATGTGCATTTACACAGCTCAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGTCGGGCTGCTCTACAAGGGCTTCACITTTCTTCCACACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTGCTGATCAGTGTGTCGTACACACATTTTACATAAATTACACAGGACTC ATACATGAAAAAT/JA/JAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAA
WI-9420	202 G A			AACITGTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATGTAAAGTCAATGACTGTGTGTTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG JG/JAGCATCTTTCTCACCTTAACCTGACGCTGIGCAAGATGCCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTTAGACTTCATTTAGAGCAGAGCACCTAGTAGAGGAATAACCTGGGAGAGAGAC TGCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGTTTCTAAA TCTCTGGCTTGGATTTATCCAAAGGCATGTTCTAACTGCCCCGIGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAAGAGACACAGCAAGGAGTTTTCCCTTTTAAATGCTAAACAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGCAATATGATCTCCCTAAAGCCCCAGATTCTCTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCAAGCTCACCAGGGCTCACCTTCCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGGACAGCCCCCTTCTTAACGTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAATCTGCTGTGAGCCATGTGCTGGCATCACAGGGT GGTTTATTAATTTCAATTTATCATCTGGACAGCCCCCTTCTTAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAAGTATAAGGACAGGCTAGAACAAAGCGTTCCCAACCCTGGCACCACATGACAGTTTGACCAAAA TAACTCTTTGTTTCAGGGGACTGTCTACACATTGTTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCAACAATCATGACAATGAAATGTCTTTAGACATT GCCAATATACCTTTGTTGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A ---	---	AATGAGTCAATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTGAAAGAGG GAAGTCTCGATAATTTAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTCTGAC COCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAAAACCGTTGGCAAGGCTCCCCAAGACTCACCACCCCAACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATATAATTAATGCTACAAATTTTCCAGTAGTTACCAGGACCAAGCCTAT TGAAGAAATCATAAATGTAACCTACAAATGATTGCTCTCTGGCTTGGTGCCAGGCATAGAGTT[G]GGCTACAAACCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTCTCTTCTTCTAAAATGTTATGATTAATTAGTGCTTTGTAGAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAATAAGTATAGTTGAACCCCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G	---	---	TGGTATTTTCCCTTTCTAAATGTTATGATTAAATAGTGTCTTTGTAAGTAAATTTGAAAAATGT AAATCAGAGAACAGAAAGAAATAAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGAATGAGAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAAGCAAGGAAAGTTAAGT
WI-5896	61 C A	---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTC/AJTA AAGCCCCCTCACACCGAGGACAATGTTGAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAAACTGGGACCAAGAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153 C T	---	---	TATTACTAGGTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAACGCTCCTCACTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGACTGTGCTC/TGTTCCCTGTGGGTCCCGGAACCCAGTGTGGTGGCACAGAG GAGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A	---	---	AGAAGACAGGAGCAGTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTGGTATACTTTCTCTTCTGAAGACCACCCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGACTTCTTACATTCGAAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATTTAGAA/GA/AAACACCTAAATGGCTCATCTTGGATCA
WI-9760	49 C T	---	---	TTTTCGTTAAGTCTTGGAAGCCACACAGAGTGATCTACTCTTTTAC/TAAAGTGTACTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATTCATTTCT TTGTCAGGAGTTCTTATTTGGCCTTCTTCTAAACCCCTTAACCATTCCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C	---	---	GAAACCTCGTTGGCTCAAAGGAACGTAG/A/C/AAATCTTTTTTTTATTTTTTAACTC AAAGAGTGGAGTTTGCAATGACCTGTGATGGCAGCTGCTCTTTGTTTGGTGATAATCCTCTAGT GGGCACCTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAAAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G	---	---	AAGCCCCAGTGGGAAAGCAGACAAACACTCCAAGATAC/A/GJAGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGCGATGTCAGACCAAAAGACATTTGGGTCT TGAGGTTGAATAGGAGTTGTCTGGTGAGCTTTGCCAGTCCCATAGTAGGTTTCCATAAATAAAC AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
WI-11152	179 C T	---	---	GATTCCTTGGACATGCAGAGCATACGGCAAGGCATCTTGGGCATTTGGAAGGAACGAGCCCTA ATTCATAGAAACAGACTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTC/A/C/TCTGTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167	A G	---	---	TGGTGAGGAGCTGAAGGCTGAAGAATAGTCTCTGCTCTGGCTTTCTGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCTCTTGGCCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGCTGTACAGTTTACTGGAAGTTGTJAGTGAACCTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGGCCTTCCCTGTAA
WI-4701	198	G A	---	---	GGGTTCAATTAACAGCCTTCCCACTGGGCTCAGATTGCACGGAGATGTAATAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAACAACACATTAAACTCTCCCCACTCTA CCGGCAAAAGTCTACCTTTTGGTTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCAATTTTCAGAAAAGCAGTATA
WI-4823	164	C A	---	---	TTTATCTTCCAAACCATTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCTTTAATTA TGCAGTTACTTGTGGCTACCAGACATTGCTTCCAATTGTAATTCCTTAACAACAGCAAGCATAACT GATGTGTCATCTTGTATTCTCTAAAA[C/A]AAGAAAGTGTCTTTTGTGCTCTGCCCCCTCTCTGT CTTCTCTGTTTCACTCTCTGTTTCCCTATTTCAGCATTCAATGATTA
WI-4860	72	A G	---	---	AAAAAACAACTTCAATTTGACATTCTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTGCTT GATTJ[A/G]GGAGATAAAACCTGATCTCTAAGAAAAATTAAACCAAGCAGTACACTAAATAGCCT TTGTGTGTTGTTTTCAGGAAAGAAAGCCAAATCCAATAAGTTGCTAAGAAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATAGCA
WI-9705	111	C A	---	---	TGAAAGGACCAGTTTGAATGCCTACCAAGGTAAAGTAAATCGGAGGGGAGGAAAGTAGGAGTTGCTT CCGGATGTTGCATAAAATTCAGGTTCTTTAAGGAGTTCCGGCTGCC[C/A]AAAAATTGTTAAACACTGATGC TGCTACAACAGCACATAGAAATCGGTGTTAGATTGCGGTTCTCTAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATGTTGCTGTGTTCTTGGTG
TGR- A004Z48	177	A G	---	---	CAAAATATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTTCATGTAAGGGTGGGCAAGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA[JVG]TCTCCAATTTTCAGGGGCTCCC GTGGGATGGTGGAGCCAAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34	T G	---	---	GGGATTCAATGTGTCTGTCTCATCCAATAAGCAQ[JVG]CATGACCTCAGCCCCATCTCTTCTTCCC TATGTTCCAGAGACAGATAAGACCTGGCCCCCTCTCTTAGGGGATCACAATATTGGAAGGATGAG GACTCCAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGAGGC TGGGAGAGGGGATCCTTCTAGTTGA
WI-7747b	88	T G	---	---	GTGAGAGCGAGGCTGAGCCTACAGAACTCTTCTGGCCTGCTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGAT[JVG]AAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTCCTGTTTGTGTTGGGTATCCCGCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCAATTTGTAATAAAGTATATAATTTTTTATGTTTGTCTGA

WI-7747a	44	T C ---			GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGC[T/C]JTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTT ATTTCTTGTTGTTGTTGGGTATCCTGCCAGGTGTTGTTGTTAAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTTTATGTTTGTCTGA
WI-7189	197	T C ---			TCCAGAATTTCCCTTCAGCTCATTTTGTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCATATTTCCCTTCAACAAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGGTTATTTTATATTAAAGCCTACAACATTTT[T/C]JAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---			AGCCCCAGCTGGAATCATGGATGTGCACCCCTTGTCCCTGCTCTTCTGCCTGG[G/A]CTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAAGGCACAGGCAAGGAGCAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---			CTCTCTTCATCCCATCACCCCTAAATAGGTGAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[C/C]JAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTTTAAAGAAACATTTGTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCTAAATTTATCTATAAAATATATTA AGCAAGTCAAACTTGGATGATCAAGGTAAATTTATTTGCAAAAGTTTAAAT
WI-7919	242	T C ---			GAAGGCAGCTGGATCACTTCCCGCAGCTTGGGAGCGCTTGTGTGGAACACAGAGCTCCTCCT CAGGGGCTGGCAGCTCACTTCTATTCTGTATGATGATATTGGTTAAACACTGTCAAAATAAGAGAT GTGCCAGATTTAGATTTTCTACCCCTAATCTGTTTAAATATTGTAACCTTTATCCATTGAAAGTGCA AGCCATTTCAGATAAGCTATAATCTGGTCTTTAAGGAA[T/C]JACAACITTT
WI-7928	101	T G ---			CTCCCTTCTATGCTCTCAGCAGCACGTTGGGCGACACTTGTTCATCTCTGACCCGTTTGTGGGCTA TTCCCTGCAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACCTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCAITTAATAAATACGTACATTTGAGGTAATGGTA
WI-7936	131	T A ---			TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTAATATATACATCTGCACTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCAACACCTTACACCAAC[T/A] ACTGAATGAAGAAGTATTTGGTACCAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTGAA
WI-7944	99	T C ---			TACAGTTCCAGCCGTTGCCCACTCATCTGCGCGCTTGTCTTTGGTTGGGGGCGAGATTGGGTGG AATGCTTTCCATCTCCAGGAGACTTTTCATG[T/C]JAGCCCAAGTACAGCCTGGACCCCTGGTGTG TGAGCTAGTAAGATTACCCCTGAGCTGACGCTGAGCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	---	TTTCTAGGCTGACAGTGCATGATTTTTTATAAATATTTCTACTCTTGTAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGGCTAAACCTGGTCAGTATTAATGTGAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	---	GGCCAGGAGATTAGCAACAAGGATTCATCTGTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTCTTGGCAGTGCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAATGTCATCAG
WI-140	252 C T ---	---	---	ATTGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTTCAATGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTACCAGTAAAGTTTATA TCTTCCATTGAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAATGTGTCATTTGCTGTATTGGCAATTCCT[C/
WI-198	218 C T ---	---	---	GAGGTCTTCAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTTCCCGGATCAAGTGTGGCACC CATGATGGAACCTCTTGCCATGGTTTGTAGTACCCCTGGACCAAGTAGTATTCCTGACCTTTAAAA TTCTAAACAGCCTTTGATGGGACAACTCTGCTAAAGACTAACCACTTCCCTATCTTATCTTCAGCTA CCTGCTCCCTTTC[C/T]GTTTAAACAAAGCATAGAAATATCTGAACAAC
WI-205c	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	---	GAAGACTGAGTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCACCTGTTTGCAACCCAGTNCCTTCCAGAGGCTCAGACTACCTCCCTCCATCTCCCCCT CTCCCCCACAAACACAAATACAGAGATT[C/AA]TTACAGGAGCCAGTTTCTAGGTGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---	---	---	AGCTTTTGAATCCAAAACCAACAT[AG/C]TTGACTCTCTTATCTCTCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCCCTGAACGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACTCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCTCTCTCTGCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---	---	AGCTTTGAAATCCAAAAACCATATAGCTTGACTCTCTTATCCTCCTCTTGTGTAACTATATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCTGAACGAGGAGGATGGGGGGGAGACAT CGGTCAATGATCAAAAGCATCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTGCTATCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTTCCCAATCCACAGGTAAACTAATAATGATGTATAGAAATTTAGAACTACTTCC(GA)GTTT TTTCCCTGGGGAAATATTCACAAAACATTTGGGTGCTGCAATCAGGTTAAAAGACATAGTGTGCCA TTTGTATCAGACAGGTAGAGGCCTGACTCTGGCAGGATTAGCTACCTAGCTGTGAGACTTTATGT ATCATTTATTAGAGCCAGGGCTTGTCTGTACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTCACTCCCAACACIATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAAATATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTCACTCCCAACACIATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAAATATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTCACTCCCAACACIATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTT/CJAAATAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATAAATATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATAATCTTCACAACTAATACCTGAGAGAAATAGTCTATTAAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATAATCTTCACAACTAATACCTGAGAGAAATAGTCTATTAAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT/GJCATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATAATCTTCACAACTAATAACCTGAGAGAAATAGTCTATTAAAT

WI-611	66 G C ---	---	TTCAAAATTAACACCATGGGTATATTAAATTTNGCTCTATCCATAGTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGCTTGACGTATTAAAGTATTCGATCAGTCACCATCTGGA ACCAAGGTTTCATTCTGCTGACCCCTCCCTCCTCACCCCTACTTGGGCTCTGACTTCCTTCTCTGGGCT GAACCTCTCTCTGTGGGCTGTCCGCCCTCTCTGCTGTGGGCTCCAAATAC
WI-681b	156 A G ---	---	TGAAGCCCTCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACITTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATAGTATGGCACCATTTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCCTTAAAGATATGCAGCAAGCAACAATCTGTCATGGTTT
WI-681	156 A G ---	---	TGAAGCCCTCTCTCTATACCCCAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACITTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATAGTATGGCACCATTTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCCTTAAAGATATGCAGCAAGCAACAATCTGTCATGGTTT
WI-667b	119 G A ---	---	AATCTTAACAGCCTTTTGATGCCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/GAJTTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-667	113 A G ---	---	AATCTTAACAGCCTTTTGATGCCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCAGTCTCCGTTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-667	119 G A ---	---	AATCTTAACAGCCTTTTGATGCCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/GAJTTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-871b	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG/C/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTTGTACCCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTTTGTACATAA
WI-871	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG/C/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTTGTACCCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTTTGTACATAA

WI-884	198 TC ---	---	AGGTTCTGGACTTGATGCTGGGAACAATTGGGTCGAGAAATCCCTATTTTGGAGTTCCTATTTTGGAGTTCCTATTTGGGACAGTAGAGCCAAATGGGAAGGTATCCCTAGTCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTCAGTGAACACATGATGAAAATGACATAAT
WI-921b	205 GA ---	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGGACGCTGCGGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCAGTCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205 GA ---	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGGACGCTGCGGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCAGTCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90 GC ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAA[C/G/C]CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCACAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90 GC ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAA[C/G/C]CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCACAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167 CT ---	---	TTGCTTCAAAGAGTCTTGTCTCAGGAAGTTATTCATTTCAGCAACCTAAAATGTTTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 GA ---	---	TTGCTTCAAAGAGTCTTGTCTCAGGAAGTTATTCATTTCAGCAACCTAAAATGTTTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 TC ---	---	TCCCACTGAGTATGGCTTCAGTAGTTTATTATGATGTGCCTAGTACATTTGTTTTATTGTTCTG CGAATTTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTCTGACCCCTTTCTGTGTTT CTTCTTAAAGATACAAATAAATGTAACATTAGACCTCTCATA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204 G A ---	---	---	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGCCAGGGTTTTACAGGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAAACCTTCTCCTCCCTGGCTC CTGAGCCAAAACAGGCATTACCATAAATCACCTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	---	GCATTGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/G/GCCAGGT TAAGTGCTGGGG/C/TTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	---	GCATTGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/G/GCCAGGT GGCTAAGTGCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	---	AAGTTACAGAAAAAATACCAGAAAAGTGACTCAAGANTCAGCTGAGATAGAAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN/T/C/GNCANT AAAAATGATTGAAATTTGGGAATAAAGCCCTCCCTCTAAATGATTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTCTTCCATT/C/TTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA/T/C/TNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTTCTGCATTGGAAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAACTTTGTGNNNNNTNG GGCTGGGTGACTGTCCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTCTCTTAA/GJGC
WI-1306	240	A G ---	---	TTTCTGCATTGGAAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAACTTTGTGNNNNNTNG GGCTGGGTGACTGTCCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTAA/GJCTCTCCTAGC
WI-1307b	118	T C ---	---	GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCAGTCTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAATTCJGTGAGATTGCTTTT CCTACCCCTCTTAAATGATCTTNCATTAATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGTTGCTGTTGTTTCTCTCTCTGTAAGNTGTTT
WI-1307	118	T C ---	---	GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCAGTCTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAATTCJGTGAGATTGCTTTT CCTACCCCTCTTAAATGATCTTNCATTAATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGTTGCTGTTGTTTCTCTCTCTGTAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGTGGCCCAAGACAAGCAGAGGGAGAGAAGAGCAACNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCCCTTGTCTCTCTTCCCTCAGAACTTCCCTGAGGGGCAGGC ATTATGATTCCTCCTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C T ---	---	GAGAGTGGCCCAAGACAAGCAGAGGGAGAGAAGAGCAACNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCCCTTGTCTCTCTTCCCTCAGAACTTCCCTGAGGGGCAGGC ATTATGATTCCTCCTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T C ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAAAGTCTGTTATTTGTAAA ACACAAAGTGGGTTTAAATGGAATCGTATGTGTAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTTCJGAAGTTGGGTAGCTACAGGCCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175	C G ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAAAGTCTGTTATTTGTAAA ACACAAAGTGGGTTTAAATGGAATCGTATGTGTAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGTCTGATACAGGCCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136	GA ---	---	TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTTGTACTTTTGTGNTGNNITCCTTTTCNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTNAATTATACCCAAAGC [G/A]GGATTGTGATGGATCTGTTTATTTCTGTCTTGGAAACAGCAGAGTCGCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTCCCGAGCCACITGACATTAGCAAGTGT
WI-1349e	192	GC ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGGCAGGTGGTAGGTCTGGCTGTCAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTAAGTACTAGATTTCAGAAAAATA
WI-1349d	264	CA ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGGCAGGTGGTAGGTCTGGCTGTCAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGTAAGTACTAGATTTCAGAAAAATATGAT
WI-1349c	192	GC ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGGCAGGTGGTAGGTCTGGCTGTCAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTAAGTACTAGATTTCAGAAAAATA
WI-1349b	264	CA ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGGCAGGTGGTAGGTCTGGCTGTCAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGTAAGTACTAGATTTCAGAAAAATATGAT
WI-1349	264	CA ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGGCAGGTGGTAGGTCTGGCTGTCAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGTAAGTACTAGATTTCAGAAAAATATGAT
WI-1403b	57	CT ---	---	TGGTATTTGGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAAATCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGCTCCTCA TAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTGT
WI-1403	58	T C ---	---	TGGTATTTGGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAAATCTTGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGCTCCTC ATAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T ---	---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGGGAGAGATGTGAGCCACCGGG GGTGACAGCATGCCCTGCTGGCATTGGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTGG GGGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGGAGCGGTTGC AGGCGAGGCCCTAGGTCGGTATTTAATGTTTGC/TTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGGGAGAGATGTGAGCCACCGGG GGTGACAGCATGCCCTGCTGGCATTGGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTGG GGGTCTCGACTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGGAGCGGTTGC AGGCGAGGCCCTAGGTCGGTATTTAATGTTTGC/TTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	---	CCATGAGCAAAAGCATGTTTCTACTCTGTGATGTATGTAGGGGCATGTATCTGTATTTCTT TTTTATTCTCCAAAAGAAATTTCAATTGCAAAACATTATCAGGCAATTCAGGCTCGTAATAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGTATGTCTTCCGTGGTACCCTCTCTCCACCACATCACCTGTGTTTT
WI-1732b	122 T C ---	---	---	TGCCTTACTTCTTTGTTTCATTCGCCACCATTACATTTTGTAAATTTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGAGGAGTNTCCCTGGGTCAACCCCTTTC/ATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGGTGCATCAGTATATCTCGAGCCTCCCAAGGTACAGC CTTTCACCTACTATTCATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1732	114 C T ---	---	---	TGCCTTACTTCTTTGTTTCATTCGCCACCATTACATTTTGTAAATTTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGAGGAGTNTCCCTGGGTCAACCCCTTTC/ATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGGTGCATCAGTATATCTCGAGCCTCCCAAGGTACAGC CTTTCACCTACTATTCATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1750	97 A G ---	---	---	GCGAATTTAATGACTCCAAAAGGTAGTAAATTCCTTTCCCCCAAAAAGGTTTTAAATCTGTGTGGGA -CATAATGTTGAATTTGCAGTTCACCTTGG/AGTTAAGGTGTGCTGTTTTCTGGCAAAAGATCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTACCTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	---	GGTACACAAAGAAATGCTTCTGGAAATCTAC/AGTJAGCGCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCCCATGAAGCTGGGCAAAAGAACAAATTCCTAGGAAAAGTACAATTAAC TGGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCOCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAGAATAATCATAAAAAT
WI-1803c	77 A G ---	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/AGJAGTAGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCTCCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAAAGTGAATCA

WI-1803b	77 A G ---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCGAGAA CCATTATGATAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATACTACTAAGCATGACTTCTAGAAAATTACTTATCTCTTGCTCTCAA GGAATGGGAATACCTATAATACAGCTTATTGAGGAAAATACTGGAATCA
WI-1837b	112 C T ---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTT AAGTTTTCATTCACCTGATGCCAAAACAAACCTCAAGACCTTGAGTGAATTTTGAGCT CGGTAAACAACITGGGAAGCTCGGGAGCGTTTAGCTTCTGCTGGCT
WI-1837	112 C T ---	---	TTTACTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTT AAGTTTTCATTCACCTGATGCCAAAACAAACCTCAAGACCTTGAGTGAATTTTGAGCT CGGTAAACAACITGGGAAGCTCGGGAGCGTTTAGCTTCTGCTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG[CTGAGAAATCTGAATATTCAGCACATACAAAGTGTGACAAACCTTGTTAGTAT ATTTATCTCCAGAGTGTTTTGAAATTTACTAAAAGTTCTTAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG[CTGAGAAATCTGAATATTCAGCACATACAAAGTGTGACAAACCTTGTTAGTAT ATTTATCTCCAGAGTGTTTTGAAATTTACTAAAAGTTCTTAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTTCTTTTGGGTTAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGAAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTTCTTTTGGGTTAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGAAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATAATGGAATCAACTGGACAACCCGNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAGAGG[CTGCTCTGAGAGGT AAAGTGCCTGCCCAACGCGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTCCCATGAGAAACCACTTTTCTTTGCTCC

WI-2013	127 C T ---	---	---	CTTTAGAGGTGGTCATTTCCGTTCCCTTCTGGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACACTGACACTTC/CTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACITTTGTTCAAGTTATGCTCCGGGGTCC CCTTCACTGGAGGATATCTCAGCTTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A ---	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTACCTACTAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATACCCCAACTGGTTTCTAGATGTACACG/ATGTGGGACCTCTGTCTCAACCTCCGACITTTAC AGATCATTGGTTAGGCTCACCITCTCTGTAATTGCTTCTGTTTTCAAAAGGG
WI-2032b	219 C G ---	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTACCTACTAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATACCCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACITTTACAGA TCATTGGTTAGGCTCAG/CTCTCTCTGTAATTGCTTCTGTTTTCAAAAGGG
WI-2032	219 C G ---	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTACCTACTAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATACCCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACITTTACAGA TCATTGGTTAGGCTCAG/CTCTCTCTGTAATTGCTTCTGTTTTCAAAAGGG
WI-2054b	188 C T ---	---	---	CGTTTTCTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCAATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/CTGCTGCCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2054	183 T C ---	---	---	CGTTTTCTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGCT CAGAGCTGCCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCAATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/CTGCTGCCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2573d	129 T C ---	---	---	TGGGATTAAACCCCTGTTTCTCTCTCCAGTTTCTGCTGCTGCTTAAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTTCCGCTTCAAGGTGTTCCGCTGCTT/CJIGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGGTAAAGCAACAGAGGCTGIGT GAAGTGAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	---	TGGGATTAAACCCCTGTTTCTCTCTCCAGTTTCTGCTGCTGCTTAAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTTCCGCTTCAAGGTGTTCCGCTGCTTGTGATAT CATCTGATCTTCCCAACAGGGCTTATTTATGCCCTAGGTAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG

WI-2573d	129 T C ---			TGGGATTAAACCCTGTTTCTTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTACAAAGGTGTTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---			TGGGATTAAACCCTGTTTCTTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTACAAAGGTGTTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2573b	165 A C ---			TGGGATTAAACCCTGTTTCTTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTACAAAGGTGTTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2573a	129 T C ---			TGGGATTAAACCCTGTTTCTTCCAGTTCAGTGTGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTACAAAGGTGTTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2868b	60 A G ---			GACTTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTTAAGAACAAAGCTTTC/JGJCTC CCACTTCCTCCCTCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---			GACTTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTTAAGAACAAAGCTTTC/JGJCTC CCACTTCCTCCCTCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 T C ---			CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTC/J AGAAATGAATAGAGCCCCATTTAAATTTATATACAGAGCTTTATGTCACCTTCTGTTCTGCTGCCATCAG TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131 T C ---			CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTC/J AGAAATGAATAGAGCCCCATTTAAATTTATATACAGAGCTTTATGTCACCTTCTGTTCTGCTGCCATCAG TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49	T A ---			TTAGCACATATCTGTTGGGACTTAACAGGACATGAGACAAGGATATAAAATTAAGACACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCTCTCATTCATCAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCCATTCGACAAATAAGTCCA GAG
WI-2954b	41	A G ---			TTAGCACATATCTGTTGGGACTTAACAGGACATGAGACAAGGCAAGTAAATAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCTCTCATTCATCAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCCATTCGACAAATAAGTCCA GAG
WI-2954a	38	G T ---			TTAGCACATATCTGTTGGGACTTAACAGGACATGAGACAAGTGGATATAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCTCTCATTCATCAATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCCATTCGACAAATAAGTCCA GAG
WI-2971b	62	T C ---			ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCCAGCATTTCTAAGAATTC/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCTCTTAAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGATTGTCT
WI-2971	62	T C ---			ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCCAGCATTTCTAAGAATTC/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCTCTTAAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAACCTTTTACTAGGATTGTCT
WI-2995d	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTINATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTJA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTINATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTJA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTINATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTJA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT

WI-2995c	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTNA /TAAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995e	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTNA /TAAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	C T ---			GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAC ATCTCACTTAGCTCCTT[C/TT]CCTGCCATATCCTGTTTTCCTTACTCCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
WI-3234b	68	T C ---			ATTCTGTAATGTTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAAGCAAGAACACACAGAAAGCCCTGTTTGGCAATCTGGCCTCTTATAAATAGTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGCAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68	T C ---			ATTCTGTAATGTTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAAGCAAGAACACACAGAAAGCCCTGTTTGGCAATCTGGCCTCTTATAAATAGTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGAGCAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A ---	---		GTTTGTGCTAGACTAGGAGTTTCAGCTTCATGCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATGGATGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCATTTCATC
WI-3292	106	G A ---	---		GTTTGTGCTAGACTAGGAGTTTCAGCTTCATGCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATGGATGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCATTTCATC
WI-3355	19	G C ---	---		CCATGAACCATGGGCTACA[G/C]ATATTCTTAACTTCAGAGTCCCTTACTGGAGAGGGATCCA CTTTTAAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTCCAGCACTTAAACCTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTTACCTCACCTTTTCAATGGAAACCTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A ---	---		CCATGAAGAATGAGTTCTCCCTCCCTGGGTACGTCCTAAGATAGCACACCTTGAGAAATTNACT TAGCAGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTTCAAGCTTT CTGGAATTGGGATGAATCTNACATTCAATGTGCACCTTCGTGTGGGATCAGTCTCTCC[G/A]TGCCCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAATCAGG
WI-3505b	131	G A ---	---		TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCTTGTATGTCATCAGTGCACCTTAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACACATTACCTATTTTNAACCAAAC[G/A] AGTGATTCTCTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3505	131	G A ---	---		TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCTTGTATGTCATCAGTGCACCTTAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACACATTACCTATTTTNAACCAAAC[G/A] AGTGATTCTCTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3564b	177	C T ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGTTCTCCAGTGTATTACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACGTGGTTGACTAACGTTAACATGCATGTCTGTTC[CT]AACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCCTTCACAAAAACAAA
WI-3564	177	C T ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGTTCTCCAGTGTATTACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACGTGGTTGACTAACGTTAACATGCATGTCTGTTC[CT]AACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCCTTCACAAAAACAAA

WI-3649	64 A G ---	---	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCCTAGTATTCCTTTAGTGGAGATTACACAG[AG] AGACCAGTTTGCCTTCACTTAGTAGGGCCAATGATAGACTTTTAGGTGCTACCACAAAGGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCCTGGCTTGGTC TTCTGTTTTACCATAATTAATGATGACATGCAAAACCTCAGAGCCTTTTA
WI-3674b	133 G C ---	---	ACAGTACACATGGCCCAATATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGCGGAGTCTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAATIG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACTTGGTCAAAATGATTGTT AATTCCTAATTAAATTGTTGTTTTATGTTTNNATTACTGCCAATCACAGCCAAG
WI-3674	133 G C ---	---	ACAGTACACATGGCCCAATATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGCGGAGTCTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAATIG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACTTGGTCAAAATGATTGTT AATTCCTAATTAAATTGTTGTTTTATGTTTNNATTACTGCCAATCACAGCCAAG
WI-3682	137 G A ---	---	CAATATAGACCAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTTAGAAACCATGTTTTT ATTGGCTCTTCTCTCTCTCTCTTTTAAATGCTCTCTCCAACACCAATTCACITTTATCTTTTCAA TIG/AJAGCATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACATTAA GCCCTGCAAAAGTCTTATGCTAT
WI-3854b	194 G A ---	---	GGTATGTTGAGTTCAGCTAATGGTCACCTGTGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGA CAAGACCAAGGACAACTGAGGACTTCTGCATGGTCTACCTGCTACCTAGGCTTCTTGATTAACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATACAGAGTCAGAGCCA
WI-3854	194 G A ---	---	GGTATGTTGAGTTCAGCTAATGGTCACCTGTGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGA CAAGACCAAGGACAACTGAGGACTTCTGCATGGTCTACCTGCTACCTAGGCTTCTTGATTAACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACTGAGGAAATCAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATACAGAGTCAGAGCCA
WI-4039	210 G A ---	---	AGCCAGCCACATCATGTTGAGTCTGCTCATTTCTCCATCTCTTATTTCTCTACTGCCTTCACTT CCATTAAACAAGAACTCTTGTAATTACATTGATGTTTGGTTACACTACAGATCCCAAGATGACCTC CCCATCTCAAGGCAACTAAATTAACACCTTAATTTCTATTGCAATCTTTGTCATTACCATTAACATATT CATGG[G/A]TCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130 T C ---	---	GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCAGATTATGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAACTCTGTCTATAATTAACCTTCTCTCTCTCTTTATTTTGGCTTC/JACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGAGGTNGGGGGTTTTCTGGGAAGA

WI-4110	130	T C ---	---	---	GAAAAATGATGTTTTGATTTCCCTCCTATCTTCAGATTATTGGAGTGTCAATAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCTCTCTCCGCTTTATTTGCGTTC/JACA GTTTAGGTAATAATAAGATGCCCAAGAAATTCAGTATTCAAGTACAGTAAAGTAGCAACCATGGG GTAGGACAAAGTNCAGAAAAAGGAGGAGGTTTCTGGGAAGA
WI-4119b	168	G A ---	---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACACTACGGGGAAGAACAGGACAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGCGCAATCAAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGCTCTGTGATCATCATCTCA
WI-4119	168	G A ---	---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACACTACGGGGAAGAACAGGACAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGCGCAATCAAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTCTTTCA TGAGACCGTCTGCAATCTTTGTTTTTAAAGGCTCTGTGATCATCATCTCA
WI-4123b	51	T G ---	---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[G/J]TTAAACTATTT CAAATAAACAAATAAGAAAAACATGATGAAATCTTCGTACATAATTGTATAGAATTTAGTGGG TTCTCCATGACATGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTCCATGCTTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTG
WI-4123	51	T G ---	---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[G/J]TTAAACTATTT CAAATAAACAAATAAGAAAAACATGATGAAATCTTCGTACATAATTGTATAGAATTTAGTGGG TTCTCCATGACATGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTCCATGCTTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTG
WI-4149b	145	G C ---	---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGCTTATAAGAAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAGCTTTCTCAGCATCTTCTATATACT GTGCTG[G/C]CTTGGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAGT AGGAGAGACAAGACAGATGTGGGGTCCCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---	---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGCTTATAAGAAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAGCTTTCTCAGCATCTTCTATATACI T/CJGTGCTGTGCCCTTGGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAG TAGGAGAGACAAGACAGATGTGGGGTCCCCCATGATATAAGGTAATTG
WI-4182	188	G A ---	---	---	TAACACACTTTTCATTTGGTTTCTCTATTACTGCAGTTAAAGGACCATCCATTATATTACAATCCCTC AGTTCTATGCTTTAGAGTNCATTATAGGACTACTGTAAATTTTCAGAGGGAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTGCAGGAGTGTGGTTAA[G/A]ATGTCTCTCT TGCCCCCTTCCCAAGTCTTAAATTCCTAG

WI-4230	93 T	---	---	---	AGACGTTGAATGGGACATCTTTCTATTTCGATTTTAGTTTAAACATTTGATAAGAATTGATGAAA GTTTGACATCCAGATTTATCTTTATAGCAGCAGAAAGTCTGGCAATATAACAGCACACTGACT TTTCCATGGTAAAGAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAAT ACATTTAAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C	---	---	---	GAAATTCATTGAATTTTGACCTTGAACTGATCTCATTAATACCTTTTNCCTGTAGTGGTGTATTT CATTTTGACAACAGAACAGACGAAATTTCCACTTAAATTTAAATCTC[CT]AAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTTATCTCTAGATATCTTCAGAACTAGGATGGAAG AA
WI-4271b	151 A	---	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 GA	---	---	---	AATCGAAACATTTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JINGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 GA	---	---	---	AATCGAAACATTTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JINGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A	---	---	---	GATGACAAATTTATGTTGTTGTCATTTTAA[A/G]GTACCATTCATTTCTTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTAGTCGTTATGCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACTTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCTATGCTTAAATGCTCAG
WI-4491	145 GC	---	---	---	ACCATCAATGTATCACCTTCTAAATTTTATAGATGATTAACCTGGCTCTGTTAAAAAATAAAAAACCT GTCTTGGACATTTGAAATAAACAATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACATA AACAAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTCA TTTCTTGTCCCATAAATAAAATTTTACATGCCT

WI-4584	144	A G	---	---	TTGGTTGGCATTAGCCCTCATAACAACATATTTACAATCATATTTGTTACTCTTATTTTACAAAACAG AAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCAGATTTGAACCCAGGAATCCATT CACCGGTACAGTGGCTACCTGGGTAAATAATGTTTAAATTAATAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAATAATAGGTGGCTTTAATTTGTTTATCAGTATGC
WI-4639	185	C T	---	---	TTTCTGCATTGAATGTGATGTGACACTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCQCTCATCTTTAAATTTGTA AATTTTAAAGGACACCTATCATAGTAATTTGTGAGGATAAAATGAAATAA
WI-5327	63	A	---	---	AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA/- JGATTACTCATAAAGCATATTAATTTTATAATATGGAATAATTAAC TAGATAATTAATAATGTGAAT TGAGTTTGAAGGTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGATGGCTCTTCGGATGACATGATGAACCTGTTCTAAGCAGACAG
WI-5390	87	C T	---	---	GCCTTGAGAAATGAAAGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTATTTTGTGTAT TTATTGTTCACTTATTTATCTGCTGCTCCCTCTGGTATGCTTGTGCATGAAACAATGAATTC CCAGTGCCTGGCCGATCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAAATG ACGAATGGTTCAAGATTGAACTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A	---	---	CCCTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGCAAGAAATCAATTTAAGCAGT GCAACATATTTTAAATTTGAAAGAACTTTGTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5404	87	G A	---	---	CCTTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGCAAGAAATCAATTTAAGCAGT GCAACATATTTTAAATTTGAAAGAACTTTGTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5545b	77	A C	---	---	TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTACCACCTCACACTGCCGCCA TATCTCTCTGAGTCCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACCCATGAATTTATTTTCAATTTCA
WI-5545	77	A C	---	---	TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTACCACCTCACACTGCCGCCA TATCTCTCTGAGTCCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACCCATGAATTTATTTTCAATTTCA

WI-5860b	134	A G	---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACITTCCTTAACCAACCTTCTAAGAGGAACCTACIA/ GJTATACGTGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G	---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACITTCCTTAACCAACCTTCTAAGAGGAACCTACIA/ GJTATACGTGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G	---	---	GCAACAACCTATTATACCTGATCCCAACCCAGGTCTACTAACATTAATCAACCCCTAACCAACATAC TATATATTGCTCTGTTCTGAATTAATTTTCAATTTAGATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTTCTACAGAG TAATTTC/GJATAGTAGGTGACCAACCAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C	---	---	AAGTAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC/ AAACCTATATTNCTGTCCTTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147	T C	---	---	AAGTAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTGTCCTTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147	T C	---	---	AAGTAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC/ AAACCTATATTNCTGTCCTTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129	T C	---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATATGCTTATTGTTAGCACCTGTC TTCCACACATGCTGTTTGTTCATATGATTCGCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGTATTGACTAAACACATACCTTGTAAATCAATAAATAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C	---	---	

WI-6244	103	T C ---	---	---	TAATTGCACAACCTTACATATCAGGGTTCTGATTGAAGGAGAGAAATATCCCTTTCTTTAGTGATT GCTTAATATTAATTCATAATAAGTGCACCATCTCTTCGCTCCCTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACAGGAGACATTTTATATACTCTACAGTGGGGGAAGACTT CCTATTTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T ---	---	---	CTGGCCTTATAATCCAAGTTTAGGATTAATCTACCCAACTTAATAGACTTCAGACAGTTGCAGTT GTCTACAAGATTTCTCTCCTAGTAGGGCTTTGGGTGTGGCACCCTTTGGCTCATTCCTCTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAGAGCTGGCAAAAACCTGCTCTTTTGCAGAAAAGAGTCG GGGTCCCAAAGATTTCGTTACGATTTTATA
WI-6336b	234	C T ---	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCAATTATGTCCTGGTAGAGCCCTTTGAGGACACTGACAGT
WI-6336	234	C T ---	---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAAGTGCAATTATGTCCTGGTAGAGCCCTTTGAGGACACTGACAGT
WI-6381	92	C A ---	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTTAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTTAACAA[C/A]GTATTTTAAAGCTCAAAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCTCACTCCCAACTTCACAATCAAAATC TACAGANGGGCAAAAGATCAGAGTTTCAAG
WI-6436	198	C G ---	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCAATGACAGACAGGAAATACAAAGGCTTAGGAAGACAGTAGTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGGTTGATAGTTGTAGTAGGTAGGTAGCGTT[C/ G]ATTGGGTGATTCACAGACAAGGTGATGTTCTAAGATTGTATTTATTGT
WI-6449	186	C T ---	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTCTCAGCTCACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTTCATCTGCAATCTCTGATCTTATGTCGTGCTCTATT[C/T]ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCAATTTTCTGTGGGTGATTTATA
WI-6449	186	C T ---	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTCTCAGCTCACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTTCATCTGCAATCTCTGATCTTATGTCGTGCTCTATT[C/T]ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCAATTTTCTGTGGGTGATTTATA

WI-6608b	46 C ---	---	---	CTAATCACAGTAGCACGTAACATGGCTCTAGTGAGTGGGCGCTCAGT[C/- JAGTTGAGGAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCACACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6608	46 C ---	---	---	CTAATCACAGTAGCACGTAACATGGCTCTAGTGAGTGGGCGCTCAGT[C/- JAGTTGAGGAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCACACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6666	68 C A ---	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACCTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGCTTACTCTGTTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGCCCTCTCTNTTCTCAAGTTCAGGCTTCTGGGTAGACCAAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G ---	---	---	AGATTAACTAATATACTGGGGCCATTGTAGGGTTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAGGGTTGTGGGGCCAGAACTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAACTTAGAAGGGAT
WI-6670	120 A G ---	---	---	AGATTAACTAATATACTGGGGCCATTGTAGGGTTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAGGGTTGTGGGGCCAGAACTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAACTTAGAAGGGAT
WI-6704c	33 T C ---	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAACGTTTACAAATAAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C ---	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAACGTTTACAAATAAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAACT[C/C]AACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAACGTTTACAAATAAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---	---	COATGGACAGTTTAATTAGGAAGCTTCGACTTGTTAGAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTGAGGCTGGAATGATCCCG(G)ATAGTAAACCTCAACATCCACACCT GCATAAACATCGCTCCCAAGTGACTATTTACTGAGTCGACACAGGATGCCAGGTGAGCCTC ATCTCCAGTCCAATGGAGAGTTGACTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---	---	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN(G)CAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAAACAGTGGAGGNGAACTTACCCAAATCCCAAGTCCCTCTTC
WI-6766	148 G C ---	---	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN(G)CAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAAACAGTGGAGGNGAACTTACCCAAATCCCAAGTCCCTCTTC
WI-6787b	97 A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTCAC(G)TTTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTCAATAGGCGACAGTAGANTACTCACAGGAAAGAGTAAATTCAAGT
WI-6793	105 C G ---	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAATCAATCAGTCAACCCCG(G)GAGTTAGAAGTAGAGTCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCGGAAAGGGGAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACAGTTTCTCATCACAGGTAAAAGGCAAC
WI-6810b	37 T C ---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTTAT(C)JAGAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTCTGTTACGNGCCAGGATAAGGCTGAACAATA AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTTAT(C)JAGAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTCTGTTACGNGCCAGGATAAGGCTGAACAATA AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	GCATGATTAAACAGTGCAGAAAAATACCAAGTACATTTGGGTGAACGATGAGTAGCTGTTCTAGTA TTTGTCTTTTGTAAATCCAGTTAAGCCATCAGCATATACAACATCACTCACTCAACAATGTAGCT GCAGGTAAC(C)ATGTGGATACCTGTGTGCTCTAGTNGCCTCCAAAGGCAATCAGGGGATCATCA AAGATGTTGGACACCTTGTTCAATCTTGTTTCAGGTGCGGCTGTGCAG

WI-6817	145	C A ---	---	GCATGATTAACACAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACAATCAACAATGTAGCT GGAGGGTAACG/AJGTGGATACCGCTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTCAAATCTTGTTACAGTGGCGCTGTGCAG
WI-6819b	221	C ---	---	GATGGAAGCCATTTATTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTCAACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGTGCTTCAACAGTTTGGCATATACAAAATTTTCTGCTATTTG CTTAGCAAAACAGCAATAACTTTTGTTTCTTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGGAAGCCATTTATTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTCAACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGTGCTTCAACAGTTT[G/TCATATACAAAATTTTCTGCTATT TTGCTTTAGCAAAACAGCAATAACTTTTGTTTCTTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAACAAATATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTTCAAGTTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT/GJGAGCTTAAATATATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAACAAATATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTTCAAGTTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT/GJGAGCTTAAATATATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACATAAGTAAATACAGCAGATGAGATGCTCTCACATGTA/T/CIATTTAAT TATTCATGCTTTTCAATAGTCTTAGTCAACTTTCAGTGAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153	G A ---	---	TTATAGAATACTTATGGGGCATACNGTAAATGAACGTCAACCTTAAATCTAAACAACAGCTTG TTTGTGTTCTGCTGAAATCCCTGCTCAAAAACAGCAGCTACTNGGTTTCTTAAAGACGTA ATTTGCAAGGCAAACTTCG/AJTAGAGCCATTCGTGCAAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGCGCTGTGTAGAACTGAGCTCATTA
WI-6909	73	C T ---	---	ATTGAAAACCTGGTTAGCAACAGATAAATTTACAATAGAGCTGGATATAAAAATGAGAGAAGATGC AGACTTAIC/TJAAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTGTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTTATTCGAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCTTATTTATACATATC

WI-6996b	242 G T ---			ACTCTAGTGCCTCTGTTACACCACCTCTAATGCCTCTGGTCGCCGCACTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTCCG(Γ)GTCGGATC
WI-6996	228 T G ---			ACTCTAGTGCCTCTGTTACACCACCTCTAATGCCTCTGGTCGCCGCACTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGT(Γ)GCTCTCTCTCCGGTCGGATC
WI-7021b	112 G A ---			TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATG(A)CCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAATTAATCAAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108 A G ---			TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATG(A)CCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAATTAATCAAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118 C T ---			GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCCACCTCCATGACAGCGCTAAACGTTGGTGA(Γ)GGTTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118 C T ---			GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCCACCTCCATGACAGCGCTAAACGTTGGTGA(Γ)GGTTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153 A C ---			AATTCGCTGAAAAAGGAACACTACCTATCCTTACATTTACCTACTAATGTCTCTTCAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTTATAGTCTATAAATAGTATTCACATCACTGTG CTTAATTTAATAGCATT(Δ)CTTATCATTTATCAGCCTTTTATGATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153 A C ---			AATTCGCTGAAAAAGGAACACTACCTATCCTTACATTTACCTACTAATGTCTCTTCAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTTATAGTCTATAAATAGTATTCACATCACTGTG CTTAATTTAATAGCATT(Δ)CTTATCATTTATCAGCCTTTTATGATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7175	194	C T	---	---	CTCTAGACTAGTGCCTTACCTTTATTATGAAGTGTGACAGGAAGCCCAAGGCAGTGTCTCTCACC ATAACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAAATCACTATATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGTTTACTGTGCTGATTTCCATGCTC C TAGAT AATTTATTTTGATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273	G A	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCAGCTGCCTGGAG AGGGTCCTGCTGTCAGTGGCTGGCTCCTAGGGGAACAGACAGTGACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTGTCACCTAAGAGAAAATTCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTCAAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273	G A	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCAGCTGCCTGGAG AGGGTCCTGCTGTCAGTGGCTGGCTCCTAGGGGAACAGACAGTGACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTGTCACCTAAGAGAAAATTCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTCAAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116	A C	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCT A C CTCTCCTCCTATTT TACTTGAGGCTGCCAATACCAAGCCCAAGTTTCAGCTCAAGAGATGCCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAAT
WI-7182	106	C A	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCC A C CTGAGCCTATCTCTCCTCCTATTT TACTTGAGGCTGCCAATACCAAGCCCAAGTTTCAGCTCAAGAGATGCCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAAT
WI-7191b	273	T A	---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAAGAGGGATAACAATGCTGATTACTAC CTTTAAAAATTTTAGATAAAATGCACAGCACACAGCACCATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTTAAGGAG CTCCCAAATGTGTACCTATTAAATTTGAACCTCAGCAAGTAGAAGACCAATTT
WI-7199c	112	T C	---	---	CCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTAGGTACCCACCGTCTGTCAGCTCCTGACCTATGAGT C JGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATAGCAATCCTTAATGTTTGTGTTTGGTCTGCTGAATTTCTTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCTTGTCTAA
WI-7199b	112	T C	---	---	CCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTAGGTACCCACCGTCTGTCAGCTCCTGACCTATGAGT C JGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATAGCAATCCTTAATGTTTGTGTTTGGTCTGCTGAATTTCTTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCTTGTCTAA

WI-7216c	237	T C	---				TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTGTTTTT/CJCTTGTAAACACTT
WI-7216b	237	T C	---				TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTGTTTTT/CJCTTGTAAACACTT
WI-7220b	147	A T	---				AGGATGATGCTCCAAAAGGGGACCTTGAACCTATTACCATTTATTTGCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATJATATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAAATCTGGCTTACTGCACATATTAGTGTTT
WI-7220	140	A T	---				AGGATGATGCTCCAAAAGGGGACCTTGAACCTATTACCATTTATTTGCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCJATJCTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAAATCTGGCTTACTGCACATATTAGTGTTT
WI-7226	232	C	---				GATCGAATTTTCAGATGATTCGGAAATTTTCATTCAGGTTATTTGTAATAGTGACATATATATGATA TACATATCACCTCTCTTCTTAATTTTGTAAATGTTAACTGGCAGTAAAGTCTTTTTTGTATCATTT CCCTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAATAATA TTACCCACAAATGCCACCAGTAACCTAACGATCTTCACTCTTGGGTTT
WI-7228b	254	G A	---				ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCCAATTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTCTGCTTTGTAACTCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAAATGTTATCCAATTAAGATATCTCAATGTT
WI-7228a	163	G A	---				ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCCAATTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTCTGCTTTGTAACTCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAATGJATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAAATGTTATCCAATTAAGATATCTCAATGTT
WI-7233c	213	C T	---				CGATCGTACTGCCAGTAGCATGTGCTGTGCTGGGCTGTTGTTGACATCCATTTTCAATTTGTTACA GATGTGAACCTTATTCCTTTGTCACTAATTATATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTCTGCGACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGTATCTTGTCACAAAACCACTGCGAGATAACGAGGGGCTG

WI-7233b	213 C T	---	---	CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCGGGCTGTTGTACATTCCATTTCATTTGTTACA GATGTGAACATTTATTCCTTGCTACTAATATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTTCTTGCCACCCTTTTGTGGCAATATTAAGTGAACCTGCTAATA GTGTAAAGT[C]TGTGCACAAAACCACTGCCAGATAACCCAGAGGGCCCTG
WI-7233	211 T C	---	---	CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCGGGCTGTTGTACATTCCATTTCATTTGTTACA GATGTGAACATTTATTCCTTGCTACTAATATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTTCTTGCCACCCTTTTGTGGCAATATTAAGTGAACCTGCTAATA GTGTAAAGT[C]JACGTGCACAAAACCACTGCCAGATAACCCAGAGGGCCCTG
WI-7238	128 T C	---	---	GGGTACAGACAGCTCACCATTGCTGTCTGTATCTGTAAACACTTTTGTCTTAGCTCTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGATAACAGGGCTATGTTTCAGTTTGTCTT[C]CCGTT CTGTTTAAACAGAAATAAAGGAGTGAAGCTCCTTTCTCATTTCAAAGTTGCTACCAGTGAT GCAGTAATTAGAACAAGAAGAACATTCAGTAGAACATTTTATTCCTA
WI-7252f	520 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252e	552 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252d	540 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252c	552 T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCAGCCCGGCCCTGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252b	540 T C	---	---	CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA

WI-7252a	520 T C ---			CCACGAGATCCAGCCCAAGCGGCCCTCCGCCCTTCCACTCGCAGCAGCCCGGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGCTCGGAGGCTGCCCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGAGGTGGAACTCAGTCATTAGACCTCCTCCA
WI-7265m	252 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCTT[//]
WI-7265l	231 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265k	121 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265j	174 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265i	227 T C ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265h	80 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265g	170 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT

WI-7265f	231 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTTCCACCAATTCCTGTGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTGTTTATATTAATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTT/AJAAGGAGTAAAGATTGCGCT
WI-7265e	227 T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTTCCACCAATTCCTGTGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTGTTTATATTAATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265d	174 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTTCCACCAATTCCTGTGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTGTTTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265c	170 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTTCCACCAATTCCTGTGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTGTTTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265b	121 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTTCCACCAATTCCTGTGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCAATTAGTATTTGTTTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265a	80 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTTCCACCAATTCCTGTGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCAATTAGTATTTGTTTATATTAATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7281b	183 C ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTGGCCAAAGTCTGGCCAGCTGGCCCTGCAAGTCTCCCATGAAGGCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTTGGCAAAAAACGGAGTCGCGAGGCCGAG GTGTTGTAAGACCACTCGTTCGTGGTGGGTCTGCAAGAGGCCTCTC
WI-7281	171 C A ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCACTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTGGCCAAAGTCTGGCCAGCTGGCCCTGCAAGTCTCCCATGAAGGCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTCAGACTCTC/AJTTGGCAAAAAACGGAGTCGCGAGGCCG CAGGTGTTGTAAGACCACTCGTTCGTGGTGGGTCTGCAAGAGGCCT

WI-7301	205 A C ---	---	---	AACTATGGCAGTGGTCTGGTTATAGTAGTAGAGGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACAAACAGCAATCA AATTACITGGACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7314c	49 G A ---	---	---	CTCTCTTTTCTTCAGATCTGCTCTGGTTTTAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7314b	49 G A ---	---	---	CTCTCTTTTCTTCAGATCTGCTCTGGTTTTAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7314	36 A G ---	---	---	CTCTCTTTTCTTCAGATCTGCTCTGGTTTTA/GJTTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCTTTTCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACCTTGTTTTT
WI-7321b	199 C T ---	---	---	ACTCAGGGAAGGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---	---	---	ACTCAGGGAAGGGATGCCCATTAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---	---	---	AGACATTCTGCTTCCCTGAAGACTGAAGAAAGTGTAGTGCAATGGGACCCACGAACTGCCCTGGC TCCAGTGAACCTGGGCACATGCTCAGGCTACTATAGGTCAGAACTCTTATGTAAGCCCTGGCAG GCAGGTGTTTATTAAATCTGAATTTGGGATTTTCAAAAGATAATTTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7336c	221 A G ---	---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATACAGCAGTTTCAAACTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGCAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTTGTGCAGAGAACAAAGAAACAGAAATCAATATAATAATTCAAAGACTATCTGCAGCTA GTGTGTTCTTCTTTACACAC[A/G]TATACACAGACATCAGAAAATCTGTT

WI-7388	94 T A ---	---	---	TGAAATCCTGGGCTCTGGCCCTGCTAGCTGGTTATTTTACTTTGCCCCCTGCCACITTTT TGAGATCCATCCTTTATCAAGAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTATAAAGCATTCACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGATTTGTGTTGA CTTGCTGCTGCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ---	---	---	TTAGATTTTAAATGGCAACCAGCACTCACTGCCACCATTCACACTGCAGATCTNCTATTCCTGG(A/G) GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAGATGTGNCATGTGCAGACAGGCTCCT TGTCTGTAGGTGTAGTACATGTACACTGTACTGTCTCACTGTACATAGTTTGTNCTGGTATTTGTTA TTGGAATGAATATCGCTTCCACTGACITTTACCA
WI-7454b	152 T C ---	---	---	CCATGATCCCCCTCCTTGCCAAATGGAGGAGCGCTGTGGATGGTACCACAACAAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTGTAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152 T C ---	---	---	CCATGATCCCCCTCCTTGCCAAATGGAGGAGCGCTGTGGATGGTACCACAACAAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTGTAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177 G C ---	---	---	AATTTGAAATCTGAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGCATAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGGAGCAACGTTCCACCAACAATTAT
WI-7464b	168 C A ---	---	---	AATTTGAAATCTGAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGCATAGC/AJAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGGAGCAACGTTCCACCAACAATTAT
WI-7464a	103 C A ---	---	---	AATTTGAAATCTGAAAAAGTGCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTCTATGTA GTACAACAGAGCCACAGCACAAAGAGGGTGGCATAGCAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGGAGCAACGTTCCACCAACAATTAT
WI-7499b	134 T G ---	---	---	CAATTCCTCAATCCAACTAGTCTGTGTCCTTAAACATTCAGACAACTTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAAGTTGCCAGAGGCACATCAGTCTTTTGAATGCTTCAIT /GJTATAGTCCCTTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATAAATTTGGAAATGAGTGATGA

WI-7499a	33	A G	---		CAATCTCAATCCAACCTAGTCTGNTGCCTAAJAGJCCATCCAGACAAACTCCACTTCGAAGGTT TTAATGCATAAGTCAGATAGCAATCCTCAGTTCGCCAGAGGCACATCAGTTCCTTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118	A C	---		TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTCTGGTCTGATTGCCTAGCJACJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGATGCAAGTAATTAATGTCAT GAAGAAAATATTTTAAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A C	---		TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTCTGGTCTGATTGCCTAGCJACJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGATGCAAGTAATTAATGTCAT GAAGAAAATATTTTAAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C T	---		TGTAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTTCTTGATGTTCCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGAACACATCCCGGTGATAGAAATGCT AAATTGTCJTGTAAGATAGGTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAAATGGATTGGTGGTGAATCTTTTGGTAGTTGTAATTT
WI-7534	135	T C	---		TGTAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTTCTTGATGTTCCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGAACACATCCCGGTGATAGAAATGCT /CJAAATTTGTCGTGAAATAGGTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAAATGGATTGGTGGTGAATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G A	---		GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCACTTGAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCCTCTTCTCTTGAJGGAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTGCTCTGCTCTTGGATGTAGTCAGTTA
WI-7543	162	G A	---		GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCACTTGAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCCTCTTCTCTTGAJGGAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTGCTCTGCTCTTGGATGTAGTCAGTTA
WI-7555c	60	T C	---		GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTCJCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTGATCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTCAG

WI-7555b	60 T C ---	---	GGTGATCAAGATCTGTCCACAGGGCTAATGCCACCATCTCCCTCAAAAATTTGTAGAGGT/CJ/CTA AAAAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGT ATAAGAAGGGAATGAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTTGATATAGTTTTCATTGATGTGCATTTGAATTCAG
WI-7555	60 T C ---	---	GGTGATCAAGATCTGTCCACAGGGCTAATGCCACCATCTCCCTCAAAAATTTGTAGAGGT/CJ/CTA AAAAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGT ATAAGAAGGGAATGAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTTGATATAGTTTTCATTGATGTGCATTTGAATTCAG
WI-7567b	290 G T ---	---	TGAGCCATCTAGTAAAGAAAGCCATTTTCAACTGCTTGAAGCTTGCCTGGGGTCTGAGCATGAT GGGAATAGGAGACAGGTAGGAAGGGCCCTACTCTTCAGGGCTAAAGATCAAGTGGGCCCTGG ATCGCTAAGCTGGCTCTGTTTGATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCTAC TCTCAGGGTCTAAAGATCAAGTGGGCCCTGGATCGTAAGCTGGCTCTGTT
WI-7569b	63 T C ---	---	AATGATCCCCCTTCGGTCCAACAACAGGAACCTGACTGGGCAAGTGAAGGAAGGATGGCA/T/C/1 AGCGTTATGTAAAAAACAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAAGTAACTGAATCCAT TGCACATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTAAATT ATTTGATGAGTTCCTACTGTATCATGGCTACCCGAGGAGAAGAGGAGTTG
WI-7574c	216 A G ---	---	GCCACAGCAGATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCTCACTGAAATCATTTTG TACCACATTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCCAGGGC/A/G/TCTGCTGGGCTGACCAAGTACTCATCCCCGTTA
WI-7574b	216 A G ---	---	GCCACAGCAGATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCTCACTGAAATCATTTTG TACCACATTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCCAGGGC/A/G/TCTGCTGGGCTGACCAAGTACTCATCCCCGTTA
WI-7574	216 A G ---	---	GCCACAGCAGATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCTCACTGAAATCATTTTG TACCACATTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCCAGGGC/A/G/TCTGCTGGGCTGACCAAGTACTCATCCCCGTTA
WI-7576c	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAA/AT/GTTGAAGGCTTATTCTACATTTTCACTAC TTTGTAAAGTGAGAGACAGAAGCAAGCAANNNNNNNNNNAAGAAAAAATAAAC

WI-7576b	168 A T ---			AATGATGATGATAATGATGATGACGACGACACGATGATGCTTGTAACAAGAAACATAAAGAGAGC CTTGGTTCATCAGTGTAAATAATTTTGAAGGGGCTAGTCTAGACACCTTTGGAAGTTTGTGT TCTGTTTGTAAACCTGGCATCTGACACAAAAA[A/T]GTTGAAGGCTTATTCTACATTTCAACCTAC TTTGTAAGTGAGAGAGACAAGAAGCAAAANNNNNNNAAAGAAAAAATAAAC
WI-7577q	77 T C ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCAT/CJCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTT TAAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAAGTTCAATTTGGTTTACAC[G/ATAGGAAGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCTGTTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTT TAAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATC[G/A]TCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AAAGAAAGTTCAATTTGGTTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---			AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAAGTTCAATTTGGTTTACAGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCTGTTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTT TAAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACAC/G/ATAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTT TAAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCG/ATCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTA/C/JACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC

WI-7577b	117	A G ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAAAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107	G A ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTGAG/GJGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAAAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619a	106	C G ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTC/GJCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	150	T C ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619c	228	A G ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	237	G C ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99	C T ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	189	T A ---			ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCAAGAC AGAGAAAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G	---	---	---	ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCG/C/GCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCATCTTTTCCCT
WI-7619j	206 T G	---	---	---	CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCT/GTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G	---	---	---	ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG ATGGCAGGAAGAAATGGGGCTTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C	---	---	---	ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G	---	---	---	ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C	---	---	---	ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T	---	---	---	ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAAATGGGGCTTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A	---	---	---	ACAAGGGGACTTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90	C G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAGAC AGAGAAGGGCCCAATGGGGTCATCC[G/C]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTCTTCTTACACAGAACAATACACATACCGAGAAACCTATTTC
WI-7619b	206	T G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T/G]TCTTCTTACACAGAACAATACACATACCGAGAAACCTATTTC
WI-7619	189	T A	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTCTTCTTACACAGAACAATACACATACCGAGAAACCTATTTC
WI-7626d	105	A G	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGCTTGGC[G/G]TTAAACCAACATCATGGACCAATGTG CCATACTAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCTGCTGTATTTATAGTAACCAITTTCTTTGGACTGTTCA
WI-7626c	155	C T	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGCTTGGCATTAAACCAACATCATGGACCAATGTGCA TACTAATGATGAGCATTTAG[C/T]ACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCTGCTGTATTTATAGTAACCAITTTCTTTGGACTGTTCA
WI-7626b	28	T A	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGCTTGGCATTAAACCAACATCATGGACCAATGTGCA CCATACTAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCTGCTGTATTTATAGTAACCAITTTCTTTGGACTGTTCA
WI-7626	144	T C	---	---	TCCATAACCGCTGATTCTCAGGCTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAT [G/T]AAGGGCAGAGTACACTGGGGCAGCTGATACAAATTTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689c	134	A G	---	---	

WI-7689b	134 A G ---				TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTTAGGAGCCAGCCAGCAAAAGGTTGTCTCTAAAJA /GJTAAGGGCAGAGTACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A ---				TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTTAGGAGCCAGCCAGCAAAAJGJGJTTGTTCTCTAA AATAAGGGCAGAGTACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A ---				TGGAGAACATTCAATCTGCCGTCACTATTCAATCAATGAAGATTAG/ACACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCCAGCATGGTAGTGGCAAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGGCCACCAGGAAGCAC AGGTCAAGGCTGGTCCACACTTATCAGCAGCAACACTGTCAGTTTCATCC
WI-7703b	164 T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT/CJGGTCTCTCACTTGTTTTTAACTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTGTTGAAGAGTTTAAAGCTTCCATTGT
WI-7703	156 T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATGATTCAAA TGCTATAAACCAAACTGATGT/CJAAAGTAAATGGTCTCTCACTTGTTTTTAACTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTGTTGAAGAGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C]A/CAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACTACCTCAGTGGGGTCTGGGGCTCGAGGCTCATCCGAGGCGAGGTGAGGAG GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743d	275 C T ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C]A/CAGGAGTCCCTGGTAATAAGTACT TACAGAAATTCGTACTACCTCAGTGGGGTCTGGGGCTCGAGGCTCATCCGAGGCGAGGTGAGGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743e	106 C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C]A/CAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACTACCTCAGTGGGGTCTGGGGCTCGAGGCTCATCCGAGGCGAGGTGAGGAG GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC

WI-7743d	275	C T	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106	C A	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C T	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743c	106	C A	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275	C T	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	106	C A	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275	C T	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	275	C T	---	---	TTAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGACACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTTCTGTACCTACTGGGTCTGGGCTCGGAGCTCATCCGAGGCGGTTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7758	144	A G	---	---	TGACATTATTCAAAGTTAAAGCAACACTTACAGAAATTATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGACATCATCAAGTG GAGAGAAATC(A/G)TAGTTTAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAAATGTGAATTTTGTATATTTCCTCATTTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCTTTGGCAGGTGCAGCCGCCACTGCGCTTTGACCTGCCTCCCTTCATGCATGGAATTCCT TCATCTGGAACCATCAGAAACACCTCACAACCTGGGACTTGCAGAAAGGTGCTAGTATGGG/CJTAGG GAAACATTCATCCTTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTATGCTGTGTG ACTCAACCAAATCACTGAACCTTTGCTGAGCCTGTAATAAAAGGTCGGA
WI-7773b	237	C G ---	---	TTAATTTACTGATCCAGCAAGACCAATCATTTGATCATAGATTATTTAAGTTTATCCGTAGTTTT GATAAAGATTTTCTATCTCTGTTCTGCAGAGAACCTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGGTTTCATGCTTTTACCCCTTTNNNNNNNTTGTAAAGTGTAGTTACCTACTTTTCTTT GATTTTCGACGTTTACTAGCCATCTCAAGCAAC/GJTTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAAT CAGATCCCAGCTTCGGCATTGTATCAGACCAACAGTGTGTTCCGGGGAGGAAACACTTTTTTAA TTACCCCTTTGCAAGCACCACTTTAATCTGTTT/CJATACCTTGTCTTATTAATGAGCGACTTAA ATGATTGAAATAATGCTGCTCTTTAGTAGCAAGTAAATGTGCTTGTCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTCTG
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTCTG
WI-7785	156	T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTCTG
WI-7789c	84	G A ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTCTG
WI-7789b	84	G A ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCATTGGAATAAACTGTCTCCCTCATTTGCTCTATGAACTGC ACATTTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATCATCATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTCTG

WI-7789	73 GA ---				TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGACCACATCTTACAGAGACTCTCCC TGACCG/GA/JTGGAAATTAAGTTTAGGGTCCCTAAAGCATTTGACACACAGTTGTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTAGTGAAGCTCCCTTACGGCCCGCTGACCTAGGATAT GCCTCCTGTGACTCGGGGCTGTCTAGACGACTAGCCAGACCCCATCT
WI-7790b	190 CT ---				AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCCTTCTAAGGTACTTCTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTCTTGAACCTC/CTTGTATACITTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTTAAG
WI-7790	190 CT ---				AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCCTTCTAAGGTACTTCTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTCTTGAACCTC/CTTGTATACITTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTTAAG
WI-7795b	81 CA ---				CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGAT/CAGTCAATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTTCTCT TAATAAGCCACATATAAATGACTTTTCTTCCAGAAAAATTCCTTGAGGAAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81 CA ---				CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGAT/CAGTCAATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTTCTCT TAATAAGCCACATATAAATGACTTTTCTTCCAGAAAAATTCCTTGAGGAAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41 GA ---				TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GA/JTTCATTTAGTCATGTGACCACCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---				TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG/GA/JTTCATTTAGTCATGTGACCACCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---				TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCATTTAGTCATGTGACCACCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7830c	54	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAAGTCTGTGATGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7830b	134	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7830	44	A G	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGTGTCACATTTTACTTTTTTGGGTGGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATCTAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATCTAGTCTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTCTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ---			CCACTTCCTATCTGATTTTCCAG[C/TAATGAGGAGGCAATTCCTAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTCAGGGTGTCTTCCAACCTGAATCTCAATGTTCTCAGTACGAAAAAC CTGAATCACATGCTATGTAAAGAAAGTGCTATTACCCAGTAACCCAAA
WI-7865	191 C T ---			CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAGATTCAGGGTGTCTTCCAACCTGAATCTCAATGTTCTCAGTAC[C/TAAGAAAAC CTGAATCACATGCTATGTAAAGAAAGTGCTATTACCCAGTAACCCAAA
WI-7867c	92 A C ---			TTCAAACACCTGTCTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATACCTGTCAAGAG[C/AGAGTCAGCTCAGGTGATTTAATGTGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ---			TTCAAACACCTGTCTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATACCTGTCAAGAG[C/AGAGTCAGCTCAGGTGATTTAATGTGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT CATTTAATATTCCCTGCTTACCCCTATTCAAGCAA[C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7868b	173 C T ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT CATTTAATATTCCCTGCTTACCCCTATTCAAGCAA[C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7868	66 T C ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT C/TTACCCCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACAC AATCATTTAATATTCCCTGCTTACCCCTATTCAAGCAA[C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTCCAGTAGTTCTATTCTAATGCCTAGAT
WI-7870b	85 T C ---			ATCTTGTCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTATTAGAAGGG GTGGGTGGCGGGAATCC[C/ATTTATCAGACTCTGTAATTAATGAATATAATGTTTACTCAGAGGA GCTGCAAAATTGCTGCAAAAATGAAATCCAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTGCGAGTGATTAGAAGGG GTGGGTGG[C]/TGGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCAGCTAGAAATATTTAAACATCATTACTGCCATC TTTATCATGAAGCAGCATCAATTACAAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C --- ---			TTAGGTCATGCGCACTCCCCAGGAGCAGCTGGCAGCTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCGGGCCAGGGCCCTCT GGCTCCCTGCCCCAATCCTCCCTGGAGAAGGACATGGGAATGAAATGGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCTCCAAGGCTGCTCTCTCCAGAGCACACAAGAAAG
WI-7889b	54 C --- ---			TTAGGTCATGCGCACTCCCCAGGAGCAGCTGGCAGCTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCGGGCCAGGGCCCTCT GGCTCCCTGCCCCAATCCTCCCTGGAGAAGGACATGGGAATGAAATGGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCTCCAAGGCTGCTCTCTCCAGAGCACACAAGAAAG
WI-7894c	142 A G ---			AGCCACCCCAATAATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTTGTA TTTACTATATCTACATACATCAATTAACATTATGTCCTATGTTTGTAATTATATTTGCGTATAC ATTATC[A]/GTATGTAATTTGCAATTTTTTATTGAAAATATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---			AGCCACCCCAATAATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTTGTA TTTACTATATCTACATACATCAATTAACATTATGTCCTATGTTTGTAATTATATTTGCGTATAC ATTATC[A]/GTATGTAATTTGCAATTTTTTATTGAAAATATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGGT GCCACAACCTGGCCATG[C]/CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C]/JACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGGT GCCACAACCTGGCCATG[C]/CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C]/JACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGGT GCCACAACCTGGCCATG[C]/CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C]/JACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAGAAATC

WI-7901	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACJTAGACACACACAGGACACATATTTAAACAG ATTGTTTCATCTTGCACTATTTCCATATAGTCATCAAGAGACCAATTTTATAAACATGGTAAGAC CCTTTTAAACAACCCAGGCCCTGGTTGCGGTGCTGGGTATTTGGGCAGCGCCGCTGGTGGT CACTCAGTCGCTCGCATGCTCTCTGTCATACAGACAGGTAACCTAGTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATTTAAACAGATT GTTTCATCTTGCACTATTTCCATATAGTCATCAAGAGACCAATTTTATAAACATGGTAAGACCGT TTTTAAACAACCCAGGCCCTGGTTGCGGTGCTGGGTATTTGGGCAGCGCCGCTGGTGGTGCAC TCAGTCGCTCGCATGCTCTCTGTCATACAGACAGGTAACCTAGTCTGCTG
WI-7928c	150 C A	---	---	CATTCCGCATCTGTCAACGAGGACGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTAAAGCAAGTATACAAACACAGATGATTTGGGAATGCCCTTCATT TACAATGCAATACCTTAC/AJATTTTAACTCTTTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926b	28 A T	---	---	CATTCCGCATCTGTCAACGAGGACGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC ACTTTGGAGATCAGAAAATTCATATTAAAGCAAGTATACAAACACAGATGATTTGGGAATGCCCTTC ATTTACAATGCAATACCTTACATTTTAACTCTTTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926	150 C A	---	---	CATTCCGCATCTGTCAACGAGGACGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTAAAGCAAGTATACAAACACAGATGATTTGGGAATGCCCTTCATT TACAATGCAATACCTTAC/AJATTTTAACTCTTTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCATAGCAGCCAGACCCACAGGCCAGGTCCTGT GCTATCAGAGGGTCACCTCTTTACAGTTAGAAAACACCAGCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTCGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCACTGCTGCCACCTG
WI-7947	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCATAGCAGCCAGACCCACAGGCCAGGTCCTGT GCTATCAGAGGGTCACCTCTTTACAGTTAGAAAACACCAGCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTCGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCACTGCTGCCACCTG
WI-7963b	145 T C	---	---	CATGTGCTGCATGAAGACTAATTTAAAAAGCAAGTAAGACTAATTTAAAAATAAAATGCC ACAAATTCATTTCTCCTTAAGTATTACAATGGAGTTTATCTGCTCTAAAAAGTGAAGAAAT TGAGTGAATGAJTCJAATTTTGTAATTTAGGATAAGATCCAAAGTATTTCCCCCACTCTGTTTCCC CCATAAAGTTAGCATTGAGGAGGAGCATTATAAGGCCAGAAAGACGGGAA

WI-8021b	57	C T	---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATCTCATCTGGAA[C/T]GATCCC ACGTCCTAGAACCTTCACCACAAGGAGTTTCTTGTAGTATTCTCAAAGTCTTGGTAGGCAATTCGA ACTGGTCCTTTCACITTGAGATTTCTTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAAGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C T	---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATCTCATCTGGAA[C/T]GATCCC ACGTCCTAGAACCTTCACCACAAGGAGTTTCTTGTAGTATTCTCAAAGTCTTGGTAGGCAATTCGA ACTGGTCCTTTCACITTGAGATTTCTTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAAGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A G	---	---	CTGAAATTTACTATGCTCTCCACAACAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCATGGCAGTCCCATGGGAAGACAGAAGAGAGT GGGCCCAGAGATGGAAGACCCCATGTCATCACCACAAACCAATTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTAGAACAGCTGGCCCTGGTCGTCAGTACACAAAGAAAGAGC
WI-8024b	206	A G	---	---	CTGAAATTTACTATGCTCTCCACAACAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCATGGCAGTCCCATGGGAAGACAGAAGAGAGT GGGCCCAGAGATGGAAGACCCCATGTCATCACCACAAACCAATTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTAGAACAGCTGGCCCTGGTCGTCAGTACACAAAGAAAGAGC
WI-8077	167	A G	---	---	GAATGAGCCTTCTAGCGCGAGGACCTGCTGCTGTTGTTGGCCTGCACATGCAATCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACTCCTTTCT AAGGAGTCTGGGTGTCATGCCCTTACAACCC[A/G]TAAATTCATCAGATGGATTTTATTAACGTT GTGATTGTGACTTACITTTCCAATCTGACTCTGGCATAACAAGGGAAGAAA
WI-8118f	114	G C	---	---	TCTAGGTTTAATCAAAGCAATTTGCANITTTGGATTTTGGATGGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---	---	TCTAGGTTTAATCAAAGCAATTTGCANITTTGGATTTTGGATGGACCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---	---	TCTAGGTTTAATCAAAGCAATTTGCANITTTGGATTTTGGATGGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGA[CT]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAC[CT]GCGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGCGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCAACGGCA
WI-8171c	46 A G ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAAC[AG]TGGCAGCAGGCGCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCAC ACATTATGGAGGGTTGCCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCAAC
WI-8171a	46 A G ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAAC[AG]TGGCAGCAGGCGCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCAC ACATTATGGAGGGTTGCCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCAAC
WI-8171b	298 T C ---			TTTCTCTCCTTCGCGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGCGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAAACAATCAACGGCA
WI-8314b	85 G C ---			GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG[CT]GAGTCTCAAAACCCAGCTCAAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACGTGTCATATGAACCTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCATATGGGGTAACCACT
WI-8314	78 G C ---			GAGGGGAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG[CT]GAGTCTCAAAACCCAGCTCAAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACGTGTCATATGAACCTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCATATGGGGTAACCACT

WI-8321	178	GA	---	---	TTTTAAATGCCCCGTTTAGAGCAGACACAGTCACAATAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTTCAAGAGCTGCTGTATATAGTCTGAGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACCTTTTCAGTATGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	GA	---	---	TTTTAAATGCCCCGTTTAGAGCAGACACAGTCACAATAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTTCAAGAGCTGCTGTATATAGTCTGAGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACCTTTTCAGTATGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	AC	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCAGCCTTAGA/AJACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	AC	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCAGCCTTAGA/AJACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTAATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTCAGATGGCAGCAGGAGAAAGAGAGAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCAATTAGA AACTGCCCCCATGATCCAATCACTNCTACCAAGGCCCTCCTCCACACACGTGGGG
WI-8378	308	TC	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTAATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTCAGATGGCAGCAGGAGAAAGAGAGAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCAATTAGA AACTGCCCCCATGATCCAATCACTNCTACCAAGGCCCTCCTCCACACACGTGGGG
WI-8426	184	TG	---	---	TTTAGCACATATTAGCATTAGCCCTCAACGATACAGCAATATGTTACATTCCTTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNNAATGTAACCTCCGACTGTGCCTAATAGGATTTGACCNTTAA GAGNTTCTTTTGTGTGGANGGGGTGGCTTGTCTGAACCTCCTCTGTTGTCCTTGTAGCTGGTG AGGCTGGGAGTATGGANGGNCOCGGGGCCCTTGGCNATNGNATCAGTGAG
WI-8450h	61	CA	---	---	TTGAGCCTCCACAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTCTATCTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATCCATTGTTATTTAAGA AAAAACCTCCCAAGTTATGTGCAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATAATGAGCAGTACAGAGCTTAATGCAATTCAT

WI-8461c	105	A T ---				CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTT[AT]NNNNNNNNCCCTTGCTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANNTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T C ---				CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAAT[CT]ATACTACAACCTTACAAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCATTTTNNNNNNNNCCCTTGCTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANNTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T C ---				CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTT[AT]NNNNNNNNCCCTTGCTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANNTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A T ---				CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTT[AT]NNNNNNNNCCCTTGCTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANNTCAAGGATTTGCAAAAAGGGGG
WI-9438	77	A G ---				AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGATGACITTAATTTTGATAAAAAAT TAAAAAGCAT[AG]AACATGCATATAAAAAATTAGATTATGTACAAAAATACCAACAGTATTTACTTC TGCTCAGTAAATTAATAATCTTCCCTTTGTTTGTCTTTTAAAAAACATTATTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101	C T ---				ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCAGTCTGTCAGCTCAGTACCTGTC[CT]GTCACACTGTACCATCTCAGTCCAGTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAACAAAG
WI-9439a	76	C T ---				ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAAT[CT]CCAGTCTGTCAGCTCAGTACCTGTCGTGACACTGTACCATCTCAGTCCAGTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAACAAAG
WI-9446b	75	T C ---				GAAGGCTGATTAAGGGAGGNTTTATTTGATGTNAACTTACCATTCCATAGACTATAAGANCATTA TAAAAAAAT[CT]CCTCTAAAGNGACACATGCCCAATGACCANGNCATAGCAACCTTTTAAAT TACTCATCTTCATATGTGTGTTTGCCCTACTNTTATCATCTGCTGCTCTTCTGCTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAAGGGAGGNTTATTGATGNAACCTACCATCCATAGACTATAAAGANCATTA TAAAAAAATG/CJCCCTCTAAAGNGACACATGCCCCAAATGACCANGNCATTAAGCAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGTCNCCCTACTNNTATCACTGTGTCCTCTGTCCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	ATTAAAAATGTCAGGGTTTCATGTTTACATTTTCTTATCAAGTACAATGGTATATATACATTTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAGTATGTTAATGTCACCT GGAATTCATACATGGAAGGCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAAAAATGTCAGGGTTTCATGTTTACATTTTCTTATCAAGTACAATGGTATATATACATTTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAGTATGTTAATGTCACCT GGAATTCATACATGGAAGGCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAGTTTTCTATTCCATCCATACATAATAGATTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTGAGAAAGTTGATCTCATCATGCGAGTCAGTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTGATTTTCCACACATTGTAC/C/AAGTG AAAGCTCTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAGTTTTCTATTCCATCCATACATAATAGATTGCTAAG/G/AJATCATTTTGGAAAGAT GTGAGCATTCAGAAAGTTGATCTCATCATGCGAGTCAGTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTGATTTTCCACACATTGTACAGTGA AAGCTCTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACACAAGTTTTCATACATCACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCTTNTAGTTGTTATGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAGCAGCCCTCTGCAAGTG G/T/C/GCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTCATATGATGGAATTCATAAACATTTATGATCCTTTTGGAGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/G/A/CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAAGGCACAAATGATCATACITCAGATTAAAATACAGGTAAGTATTCAG GGNTAAAATGGTACAAAAAAGGCTGTAACTCTTTTNCITTCACATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGTACCATATATTTGATCTNCTCCTTGGGAAAAACCTTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGGGACAAAGTACTCTG/TGTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTGGGAAAAACCTTTGGAAAAAATGAAACACGCACA TAAGTATCATAACTGAGGTTGTGGACAAGTTACTCTTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTCTGAGATTCAAGAGCTACATTTTGGTTAGTGTATGTACTATACCTTTTTTCATCCTTTCA ACATCTTTTGTGCACATTTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAAGCT TACAACTTC/TGTCTCTTACCTGATACATTTATCCATTTACTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGCTCCCTGCTTTTGTAGTTAATGTTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCA/GATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGC/GT/CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGAAGG C/T/CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTC/CCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC C/AATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATGAGG C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC C/AATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---				TGGACCAACACAGACAGATGATATCCTGGTGCCTGTGTA(C/A)ATTACAACTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACAIGTGTATGCTGCC
WI-9738	40	C A ---				TGGACCAACACAGACAGATGATATCCTGGTGCCTGTGTA(C/A)ATTACAACTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACAIGTGTATGCTGCC
WI-9756	47	A ---				ACTGAAATGTAAATGGCCAAAGGCCACCCAGGACCTTAAATCATAAGAAATTAATCTGTGGGAAA GAGTAACACTACAAAAGCATCTAAACAGAGCAGGATGTGATGTAATGTGTCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGGTATCCACTTCCACAAACACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCACTTGATCTTCACTTTTTATGATTTAAACCTCCTGGGG
WI-9758	135	A G ---				GATGTCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAGAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATCAAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/GTAAATAACTCTGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAAACCGCTGGTTTCTAAAT ATTACG
WI-9778	127	G A ---				ATTTAAATCCAGGCAGCGGGGAAAATGGATACTTTTCATATGCTCTGTACCAACTATAAACTTTTG GTTCTCATGCACCAATTTTCAATTTTGCCTTCTCACTCCAAGTACCAGTGAATTTTACCAAT(G/A)CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGAAATTTCTATTTACACACTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---				TCCTCCCTTTGCTCTCATGCCACTCCCTCAGGCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTT(C/A)TGGATCCCACCCAGGA CTCAAAAACACTAGGAATTTGGGAGAGAGGACCTGGAATCGGTGTGCTAGCAAGCCCCCAGGTGG TTTGTAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTGGCTTTGGC
WI-9841	101	A G ---				TGGAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC(G/T)GTGATGATATATACATTAAACACTT AGGATTATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATATGCTGTTG
WI-9880c	222	G A ---				GAACTAACACTTCTTCATGGAATTTTCTTGATTTGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTGGATTTTATGATATCTCTGTAGACCCATAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATAAGATCCTCTTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA(G/A)TTGACATAGGAATTACCTACATATTTG

WI-9880b	157	C A	---			GAACAAACACCTTCTTGCATGGATTTCTTGATTAATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/AJATATAAGATCCCTCTTTAAATTTATATTTTATAAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---			GAACAAACACCTTCTTGCATGGATTTCTTGATTAATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCCTCTTTAAATTTATATTTTATAAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T	---			ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCCAGTTATCAGAGTTCTNTTTTGTTC/TTACCC ATTTCCATAACAAAAGAGCTACACAAAATTTGGGGGAGANACTCTCTTTGGAGACTGACACATTT TGCAGAGGGTCAATGAATAATGATTCAAA
FB25G10b	109	A G	---			TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAATGTTGATTTTAGATCTCCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCC GGAC
FB25G10	109	A G	---			TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAATGTTGATTTTAGATCTCCCCCAG TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCC GGAC
IB3071	102	C A	---			ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTTAAGNTAAATAAAATAAAATTC/AJCAATTTAGNAACAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C T	---			CGTCCCTTCCCTTTTGGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGTTGTCC TACTGAGCTTGGGCCAGGTGTGACTTAGGAACCCCAATCCCAAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGTCT/TTGACACATACATGCGGCCATTTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTCC
S72904	51	G T	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTCTCTTTGTTAATTTGTGAGTTC ATTCTTGAAAATCTTTTGTAGTTAAAATAAGGATCTTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTCCTCAAAACCAAGTGTGTAACCTTCCCTCTTCTGTCAATTTGGTTGTCTTTAAATA TTGCAAAAGTCTGTGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTGGTTAAAGACTGAATTTGTAAACC CATTGAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGA[C/T]ACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	COCTGTAGCAGTCTTCAGCCTCCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTGGTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAAATTCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGTCACTTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAACAGTTTCCITTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTCTCCACATGATACNTAAGTTCAAGGTCCAAGTTCCTATCACAAATTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAAATAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGCTAAATTACTGCCTTAGCAAACNCIATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTTGGCTCTGTCCTCANAGTCTCTCTCCATGTTGGCAAACA
ESTC139	45	---	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTGACAGATTTCTCAGAGGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCCATTTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCAATTTAAATC AAAGANACCATTCATTCTCTAACAACA
ESTC143	29	---	---	---	---	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTGTAGCAGCATTTTCGG
ESTC146	20	---	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	---	TCITTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGNATGAGGGCCTGTGGAGGCCCTCG GGGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTCTTCAGTGAICTT
ESTC150	20	---	---	---	---	CCAGGAAACAACAAGCACACANACTTATAGAACTATTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCATTTTCTTTTAAATACAAATCTACTGGTGTCTNAAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCACGAATTTAAGTGGATCAACAATT ATATTATTGATAACAACCTCATGAGCATTTTACA
ESTC156	32	---	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAANCTGGCTCGGATGGAGCGGGGGCGCCTCA CCACCCTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCTGGGATTTACTGCTTGTATGACTACANGGCTTTGACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCTGAGGACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTGCTGCCATGAGCCNCAAGCAGCAGCATGATCATCACCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGTGTCAGTGGGGSCCTGAGCTGGGNGCAGTCGGCAGTGTCACTGGGCCCGCTTGG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTCGTCGGTTGCAAGTTGCTGTTGTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATATTGGTTTGTAAACANCGAATACAATCCAATATATAACATTAACAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAGGTGCCCGCTCTGTTCATGACTT
ESTC176	23	---	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGTGGCTCTTAAATACCTTCCATTATATTTTCAAAATTTTNCITTTATTCTATTAATAACCTTTTAT TCTCTTTATCCCATAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTTGCTCCTGTCAGCTCCCTGCCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCAGGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCTCAGCTTG ATTTTACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGCTGGATGCCAAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTAAACAGGGTTATGTACACACCNLTGTCAACCTCAAAACAGATGATACATCACTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAAGTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACITTCCTTAACCTTATCAGTCTAGTAAGCNTTTCAAAAGGAGGAAAATGGGTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCCNCGCAAAGTCTCCACAAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTAACAGTACTTTAAAT CAATTACTCTTTTGGCTGCAACAG

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCACTGACNTTTCTTCCTCTATCCCTATAAAATAAGGAAGCAGAAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATTTCTTGAGCCGCTTGTCAGGTTTGATTCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTGGTGATCATTTGTAATATACAAATACAAAGCAATTCCTCAGA
ESTC33	25	---	---	---	AGCACTTCACGCTCCTTGACGTTGNGGACCCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGAAAGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCAITTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTATGCTGATGGAAAGAAACCATTT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTGCTGGAGTTTGTCTTTGTACNCCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGCCGTGGTGAGCCCTGCCGCTGCCATGGGCCAGGAGCCACTGGTGGGANGCGGGCAGATGTTTACCCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCAAGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCNCTCTCTGGGCACAGATCCCAACAGCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGGCCCCACGGGAGGGTGGGGAGACGACACTTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCACACACTTACTTACTGCTCATCCGTCACITTCGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGTGTCTCTGAGTTGCANGCAGATGGAGATTTGGACACTG

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGCCAGGAGGCTGGCNITTTGGCGTGACGCCTAAAAAGTGTGACC
ESTC74	49	---	---	---	AACAAITTCACAGCTACAGGAAATCTAGAACAAAATCAAAATATTCATCNCNTTGGGTGAAAAAGTTG
ESTC77	40	---	---	---	GAAGA ATGACTTTCCTGTCCCATCGGAACACAGAGTTTCCCCAGGNGAGCCCTTCTATCTCGGGTTA
ESTC81	20	---	---	---	GGCTCAGCAGAGGGATAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGNTCTCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA
ESTC83	53	---	---	---	GAGCCTGACCCA CAAAATCAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC
ESTC85	28	---	---	---	TTTCACAAACCT TTTAGCTGTATACCAAGTTTCCATAAANCTGTCTGTGTTGGGAGGCTACAGCCTGACCACATTCT
ESTC89	22	---	---	---	TTTGC ATTGCAAGGAAGTGAACGCTGNTCAAACACAGAAAATGGTGACAAATGA
ESTC90	33	---	---	---	CTGGTCTCTTCGCTTGGCAITCGTCTCTCTCNGGCCAGTGTCCACCCCAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCTCTCAGTTCACAGTGGAGACTANGGAGATTACAGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCCTCTCCAGAGTTGNAGACGCTATTTAGTTTGATTCTGTCTG
DWU-100	127	C	T	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGTGACTCCTAAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTCTGACTGTTCTCCA[C/T]GCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAGATTCTGGCAAGCAGCATCTAGAGATAC ATCTTATTGCGATTTTCACAAAATCAAAATCAAAAGAAAGAAAGGCTTAGCTG
DWU-177	77	A	G	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAAGACGCTTGCTGAA TGTTTCATGGC[A/G]GCCCTATTCACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATTACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGTCCCTACTACACTGTGGAT
DWU-286	213	A	C	---	CAAAATCCTGGACTATCAACCTTGTTGCTTAATCCCTGCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGTGAAATTCACAGGGTCCACCCCAATCATGCCAGCTTCTGTCAATATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/C]TGGGAAACCCAGCCCTATCTGAGTCTTGGCTCCCTCC

DWU-252	94	A G	---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAGGAGCTACAAACCTACCTCA[G]TGAGCATGGTACTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C T	---	---	GAACATTCCTCTGCAGCACCTTCACTACCAATGAGCATTAGCTACTTTTCAGAATTGAAGGAGAAAA TGCAATTATGTGGACTGA[C]TCGACTTTCTAAAGCTCTGAACAAAAAGCTTTCTTTCTTTTGCAA CAAGACAAAGCAAGCCACATTTGCATTAGACAGATGACGGCTGCTCGAAGAACAAATGTCAGAAA CTCGATGAATGTGTGATTTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A G	---	---	GAAAAATTAAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAGGCCAGCTGAAGAGTAAAGGAAAGGCTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGCGGTACCAATTCAGTGTCTGTTCTTCTTCTGTC
DWU-1537b	89	A G	---	---	CTCTTAACCTTCAGTTCCCTCATCTATAAGAAATAGGGATTTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC[G]TGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	---	---	CTCTTAACCTTCAGTTCCCTCATCTATAAGAAATAGGGATTTCAGTTGTGATCA[C]TATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAAGGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACCTGAGCTG[C]GAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-ADAA	184	G A	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAAGGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTC[G]A]GCACCTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-ANT1	160	T C	---	---	TCTCCTGTCACTTCTACTCCTATTAGTTCAGGTCAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTGCGAAACAAGAGGGCGCAGTGGAGAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCCAACTGAGGCTT[C]GAGCTCAGATGATCCTGT
EST10398 2b	168	A G	---	---	TGCCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTTCTTCGGGCCAAGAAGGTATCTACC[G]ATAGTGTCTATTAGGCATTG

EST10398 2a	147 C T ---			TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGTATGATGTTGCATTTGGGGCTTGACCTTCCAAACAGGGAAG CATTTGTTCTTTC/TGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA/GCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTC AAGG ATAATGGGGCAATCATTCTTTT/CCTCTTTAGAGCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTACCG/GA/CAGGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACCTCTATAGTGGGTCG TATTCTGTCACAAA/A/GTGCATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGG/GCTGGGGCCAGGCTCACCTCTATAGTGGGG TCGTATTCTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGCAGGAGGTGGGAGGGGGTCTGCTCTCCAGGTCCACAGACCAGAGAGCGGCTCAGTG TATCCCAACCCCA/A/GTGGGGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCACTTTAA/A/G/AAACTTTACCGGAGAGAAATTAATAATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAACACAGAAAGGAGGATGTAACA
EST36751 7	36 C T ---			CCAAGTCGTCAATTTAGCTTTGCAGGTTTAACT/C/TGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACITTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAAATCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCA TTAATAACAAAT/A/GTTTTACCTTTTGA AAAATAA ATGAAGGATTTGACCTGCTTGGCTCTGGAAGAGTATCCGTACCGTCCCTGACGTTTTGAACAATACA GATGCCCTCCCTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121 C T ---			GCTCTATACCCCTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGAAGACTGGCTGCTCCCTGA/C/TGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT/C/TTCAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A/G ---			AATCCAGCAGCTTTAGGAGGCTGAGGAGGATATACCAGAGGTACAGAGTTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCGATGGTGGTGCATGCCGTG AATCCAGGAGGCTGAGGAGGAGATCGCTTGAACCTGGGAGGCG/GAGGTTGTGGTGAGCCGA GATGGCACCATTTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC

EST70523 3	182 G T ---			TTCCGGCAGCCCCCCTTGGACCCCTGGTCCCTCAGGGGCCACCCGCGGCACCTCACCGCTCT CGCTCTCGGTAAACATCCGGCGCGCGCTCTTGGACATAGCCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCGCTTCTGTCCCGGCGCTTGCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTC
ESTD- APOA2	101 C T ---			CCAGGTGTTGGCACGTCCTGTATCCAGCTACTCGGGAGACTGAGGCATGAGAAATCTTTGAAC CGGGAGGGGAGGTTGCAGTGAGTGACATCGTCGTCGACACTGCACCTCAGGCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---			CAGTGTATCTGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTTGGTTACAGGAGGCTTT AAGTTCAAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCTCTAGAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTGTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTGCTAAGAACCTT
EST74167 6	137 C ---			AGACATGAAGGAGTTGAAGGCTACAAATCGGAACCTGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAGGAGCTGCAGGGCGCGGCGGCGGCGGCGGACATGGAGGA CGTGCGGCGCGCTGTGTCAGTACCGCGGCGAGGTGCAGGCCATGCTGCGCCAGAGCACCGAGGAGC TGCGGTGGCGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C ---			CGCTGGTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCGCGATGCGGATGACCTGCGAGAACGCGC TGCGAGTGTACAGCGCGCGCGCGCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG GGCGCGCTGGTGAACAGCGCGCGCTGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
ESTD- ARSB	126 A ---			GGAAGAAATGGAGCTGTGGGAAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCGCCCTTGCTGA AGCAGAAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATGAGCTGCTGCATAATTTGACCCCAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACCTGCATCATCAATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCGCTGACCAAAATATACTGGGTTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATAGTCTTATTTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ---			TAATGTAAGCTCATCCCAAGAGCGCTGCACCATGTTTGGTTGAGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATCTCTGACGACTTCACTACCAAAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGAGCTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGAACAAGACAAAGCAAGCC
ESTD- BA511	29 A G ---			GGGCAACATAGTGAAACCCCATCTCTACA/GIAAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGAGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAAGCAAGATGGTGGCACTGCA

ESTD- BCL2	116 A G ---	---	---	AGCTGGATTATAACTCCTCTCTTCTCTGGGGGCGGTGGGGTGGAGCTGGGGCGAGAGGTGCGCGTT GGCCCCCGTTGCTTTTCTCTGGGAAGGATGGCGACGCTGGGAGAAC[A/G]GGTACGACAAACGGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTGCGACAGGGGCTACGAGTGGGATGCGGGAGATGT GGCGCGCGCCCGCGGGCGCGCCCGCAACCGGCACTTCTCTCTCCCA
ESTD-BCR	69 C T ---	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGAGAGCTCATCATCTGCGCAAGA GA[C/T]CAAGAGGTCAGCTTCTGTGTCGGGAAAGGAGGAGGTGACAAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTGGCACA
ESTD- BRCA1aa	119 C T ---	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTC[A/C/T]TGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCAGCTCTAGGGAAGGCAAAACA GAACCAATAAAT
ESTD- BRCA1bb	139 A G ---	---	---	ACTAAATGTAAGAAATCTGCTAGAGGAAACCTTTGAGGAACATTCATGTACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAATGTT TTAAAG[A/G]AGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD- BRCA1cc	126 A G ---	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTAAATAAGGAAGATAC TAGTTTTGCTGAAATGACATTAAAGGAAAGTTCTGCTGTTTTCAGAAAAGCGTCCAG[A/G]AGGA GAGCTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGCCA AGAAATTAGAGTCTCTAGAAAGAGAACTTATCTAGTGAGGATGAAGGCTTCCC
EST51212 0	122 A C ---	---	---	ATCCTGAGCTCGCCAAATAAGCTTCTTGGTTCTACTTCTCTCTCCAGAGCCCCAATTTCACTTCTCA GAGGAAATCCCAAGCTTAGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACA[A/C]AAGGGCCCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGGTGGGATCCTCTCCCT[A/G]ATTGCTCGGGGAAGCACATTTCAT CAA
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGGTGGGATCCTCTCCCT[A/G]ATTGCTCGGGGAAGCACATTTCAT CAA
ESTD-C6	31 A C ---	---	---	CCAGTCACTTTGGGGACAGCCATGCACCTG[A/C]GCCTCTGTGTAGCCCTTCAACCATGCATTCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---	---	---	GTCCGAATCCTCCTCTGAAAGTGCCCGGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGGTTTAGGACGCGGGTCTCTCGTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018: 6	67 A G ---	---	---	ACAAATCCAGGTACACACATTCCAGAAAGAGGAGGGGTGGTGCAGTGAGCCTGGGTAGGTCCAGTAATCCA [A/G]GGATTGAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T	---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCTTGGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGAACCCCAAGCAAGGAGACCT AGTAACATAATTGCTTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C	---	---	TAGAACATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGACCTAGTAACATAATTGTGC TTCATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAAAAACGTGTCCCAACCCGA GGTGGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145 A	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAAGTGTCCACCCGAGGTGCTGTGTTGAGCCATCAGAGGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACCAAGTGGAGCTGAGTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACAGACAGACCCCGACCCCTCAAGGAG
ESTD- CB25	146 A G	---	---	GTTCCTTTCAGACTGGCTTACCTCCGTAAGTGAGTCTCTCTTCTCTCTATCTTCGCCGTC TCTGCTCTCGAACCCAGGGATGGGAATCCACGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTGAGCTACATGCTCTGTTCTTGTCACACAGAGCTTACCAGCAAGGGTCTCTCTGCC ACCATCTCTATGAGATCTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD- CB27	125 C T	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTGCATTCAGGAGTGTCTGTGGAGTGTGCTCATCAGTGCATGATCTTC TGATTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCCTGTTTCATCTGATGGAAGTCTCTCAACACCCATTTCCATACC
ESTD- D4S338	59 A T	---	---	TTTTCTGTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/ATATGTA TTTCTTAAACAATAAATCTGAAAGTCCAAAATTACTCTTGATCCATGGACTGCAGAATAAATGTTA TTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G	---	---	CAGGCCAGCGTGGTGGAGGTGGTCAACCATCCCGCAGAGAACAGGTCAAGCCACCTATGCA/GJCA GGTTCATCATTTGAAGCTGCTCTCAGGGTCCCTTGGCCTGAGCAGGGCGGAGGACATCTCGG AAAAAACATTTAACACCTTTCAATCATATACACCAATA/CJATTTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAATTACTTGAATCTAAATGTCAATACTGATTGATTGCAAGTTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D11S1873	40 A C	---	---	CATCCCCAAGCCCATCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGSCCGT CATGCTGCACACATCCAGGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCGGTG GGGTGTGTTGGCTATGTTGGTCTTGTGTAGAC/CTGGGGGCTTGGTTTTCAGTTGCACATTGCGT ATTGCAGATTGCTTGTCTTCCACTGAGCGAGCCTC
ESTD- D17S33b	169 C T	---	---	

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ESTD- D17S33a	75 C T ...	---	CATCCCCAAGCCCATCCTCTAGCCACTGGCATTCTTTGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTAGTCATGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGGCTATGTGGTGGTCTGTGTAGACGGGGCTTGGTTTCAGTTGCACATATTCGGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ...	---	TTTGAGACCACCTGGCCCAACATGGCGAAATCACATCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATTCCTTGAACCCQA /GJGAGGCAGAGCTTGAGTGAGCCAAAGATCACACCCTGACCTTACAGCCTGGGTGACACAGTGGA GACTCTGCTCAA
ESTD- D3S11	44 G ...	---	AACCTGATTAGAACCTGAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAATAAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATCAAACATATTTATCACATTAATTTATTGGTAAGCCATACTAAATTTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ...	---	AGGTTCCACATTATTGCTGATGTTTCTGATGTTTCQAGJGGAGCCTTGATGTCATTCTGTATCTCCT CAGGTATCCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTAATTCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ...	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATACCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCCGTTGTT
ESTD- D3S2a	248 G ...	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATACCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCCGTTGTT
ESTD- D7S399	83 A G ...	---	TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGJGIGTCTCCTACATCATCCTTTACAAACATTTTCATCCATGGACTCCATAC TAGAATATTGAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ...	---	GTGGGACACCCAGGGCTCCAGGCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGAGGAGGAGTGGGGAGGAGACA GAATGCTGATTJACJCTGTGGTGGAGAACCAAGAACTCTGGCTGTGGTAGGGGAGCTGCTTCCAAG ACCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAT
ESTD-DMa	66 C G ...	---	GTGGGACACCCAGGGCTCCAGGCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT GJTTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGAGGAGTGGGGAGGAGAGA CAGAATGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCCTGTGGGTAGGGGAGCTGCTTCCAAGA CCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAT

ESTD- DRD1	154 C T ---			TCCCAGCCCTATCGGTATATGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAOCCCATCAC ACAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTCTCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGG[C/T]TCGTATTAGAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCTTGGTCAGGAGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCACCAAGCTGACTCTCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCGCCCAACACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGCGCATAGTAGGCTGGCGGGCCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGATTTCAAGTGG[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCACAGAGGAGGTGCGTGATGCCAAGGGCTTCTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---			TCCTTCAGGATCCGCATCTGCGCCTGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGGTGGTGGTCAAGTGC[T/G]GGGGCCGGTGCAGACCCCGGGCTGGGAGGACTTCA CCCCGCTCACCTCCGTTTCTGTCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	43 A G ---			ACTCACAGTCTTTAAGTAAATGGTCGAGAAAGAGGCACC[G/G]GGAAGCCGCTCTGGCGCCTG GCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTTTCAGAAAGTTAGTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAGTATGATGTTTA[G/G]TCAAACCTTCATTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGCAGCTCATGACAAATTTGAAGCTGACAAATTACACAAGAGGAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAACATTTGAAGTTGTTTTGAACTTGGTGTCACTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GCDH	200 C G ---			CGCAGACCGGTCAAGTGGGGTCGGGAGTGTGGAGGAAGGAGGGAACCTGGGGGTTTAGGGACT TTCGGGGTGACTTTCCCGTTCTGTCTTGCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGACCTCTGGTGCACCCGTGTCTGTCTGCCCTTTCAGCTGTCTGTCTGCCGAGT[C/ G]GACTCTGTCCCGAAATTCGAGAGCT
ESTD-GCK	88 A G ---			GTTTTATGCATGGAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTGCTGATCACCATGAC AACCACAGGCCCTCTCAGGA[G/G]ACAGTAAGCCCTGGCAGGAGAAATCCCCCACCACACCTGGC TGGAGCAGGAATGCCGAGGGCGCCTGAGCCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCCTAATTACTCAAAAGCTGTCCCAGGTCACAG

EST34088 2	62 A T ---				GTGGGGCAACAGTGGGAGAGAAAGGGCCAGGGGTATAAAAGGGGGCCACAAGAGACCGGGCTC[A/T] AGGATCCCAAGGCCCAACTCCCGAACCACCTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---				GACCCGTAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACAC[A/G]GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAAATTCAGGTAAGTGATGGTTCCCTAGG
ESTD-HT2	154 G ---				GGGCTAAATTTCCGAGCAACTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGATAAAAGGATAACCTGGGTTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ---				AACACAAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGGTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGTCTGCTGTTGGTTTTCTCTTCATCTATAGATTGATTGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTACAAAATGAAA ACATTTTCGTGCTGTGTAATCCCTCGAAAAGGTTCT
EST37382 5	124 A G ---				CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCTCCCTTGA CTTTGAGTCAAAATTTGGCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAAGG[A/G]CCCCAGA AATCACAGGTGGGACGTCGCTACCGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATTCACGGTCTTGGCAGGAGTG[C/T]CTGGGAGAAGAAGGAAGATG TTCCAGGCAACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---				TTTACTATTTCAATGGATACAGAAATTTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCCTACATTGTGAGTGACGGGGCAGTGGTGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAACCCA
ESTD-IL1A	110 A G ---				CAAAGTAAGCACCACAATAATGTTAGCTATTACTATCATTAATTATTATTTATTTATTTTGTG AGATGGAGTCTGGCTGTGTCACCCAGGCTGGAGTGCAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCCTCTGGGTTTCATGCCATTCTCTGCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	99 A G ---				CCACTACAGATGGATAAATGGGTACAAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTACCTTGGGTGCTGTTCTGCTGCTC[A/G]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---				TCCAGGTGGCTGGACCCAGGCCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTGTGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGAGGGCACTGGCCCTCAGCTGCCTCAGCCCTGCCTGCT[A/ T]CCAGATCACTGTCTCTGCCATGGCCCTGTGGATGGCCCTCTGCCCTGCTGGCGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGC

EST45311 0	151 C T ---	---	GGCCCTCCTCTCTCCAAATCTGTCCCTATAGTTTCCCTCTATTAAAGTGAACATACATGCAATCTTTTAGT GGATAGATGGACACAAAGACACAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAAACA CATTTTCTGCAATC/TAACCTCTTTCAITTAACAGCCCTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTGTGAAT
EST65258 8	80 A G ---	---	TGCCCCATCAGCGCGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCJAGJCCCTCAAATGACAGCCATGGCCGGCGGGTCTTCTGGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCAGCTTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---	---	ATGCAGGATGAAGGTGGACAGGGAGG/ATGAGGGCCAACTGTCTATCCCGGGCTGCAGATGTCG CTGGACTATGGGTTTGACCCCACTGACCTCCATGAGCAATCAGGG
EST62782 149 G T ---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAA TTTTTTTCTCTG/TAAGTGCCAGTATCCCGAGATTTGGTTTGAACAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTCTGCTTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TTTGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGTTTTTCCATTAAACCACTATTACTTCTA/TA GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---	---	ACCCTACCCCTCCCTTAGCCCGTGGGAAGCAGGAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/CTGTGCAACATTGACACA
ESTD- KRT8a	21 C T ---	---	ACCCTACCCCTCCCTTAGCC/CTGTGGGAAGCAGGAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCCATA GGCTGCCTATCTCTCCCGTCTCAGGTTTACCAGTCAACATTGACACA
EST75099 6	82 C T ---	---	CACCTGTGTGTAGATCTCCTCAGTGGCGGCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/CTGTGGGGCAACCGGAAGACCATCTTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCTGGCGTCTTTGAGGTGTGG

ESTD-LF79	142 A G	---	---	GGGTGATTTTGAGGCTCAGTTAATATTTCAAATTTGTAACGCTAGCAAACTGCATTGGTATTAGA AAAAATAAAAAATTTCCAATATGTAGTGCTGTGTATACCTGCCTCGCCATGCAGCATATAGCCTGT GGGAACCTAGGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCTTCCACCCGATG GAACTCCCGGCAAAATCCTGACACGCTGTGCACCCAGGCTGTACCAATATTAGTGAACATGGCTTCGAG AGAGTTGACACAGATTCTCGGAAGACAGACGCGGGATGGGGCAGGAGAAAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G	---	---	TACACACTTTCCTTACCCATTCACTGAAACGACTGCGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGCCTGTCCCTGCCTGCA AGGTTTTCCTTAACTCAATCAATGCTCTCATCTTTAGCTGTGGGTTTGTGTTG TTCCTGTTTTCCTTAGTATCTGACTACCTTTTAAATATAAAAGAGATGTATCTAAACAAATAG AGATTGTTATCAGAAGTTCACAACTTATTAAAAATTTTTCACCTG
ESTD-MCC	45 C T	---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCTCCAGCTCTGTCCCTAGCCTGAACTTCAGGACACGTGC AG
ESTD-METH	118 C T	---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTGCTTCCCAAGGTTTGGCTAAGTGTGATTACCTGCTGATTTCTGACCG ATCTTCACTGCTAGAGCATCTGGTCTCTTTTAGCAITGG
ESTD-NF1	25 A G	---	---	ATTATCCAGATGAATTTACAAAATGATGTTACAGATCCACAGACTGATATGGCTGGT AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGTACTTATATCCACTGCACACTGCTGCTAGGCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAATCTCTTTAAACCTCACCTTTGTTGGGGTTTTGGAGAAAGTTATCA
ESTD-NPA	107 A G	---	---	TGTCCTTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTCTGCTGCTGCAAGAGAACACA GACAT
ESTD-NRAS	45 A G	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTATTTGGATACCTTTTGTGTTGATTATATATTAGCAATTTGAGGG ACAAACCATAGTAGGCAAGAAATGGCTTGAATAGTTAGATGCTTATTAACTTGGCAATAGCATG CTTATCTCTGTGGTTTAAATAAAAT
ESTD-PAI1	202 C T	---	---	GCCACCAACCCACCCAGCAGCACCTCCACCTCAGCCAGACAGGTTGTTGACACAAGAGAGCCG TCAGGGCACAGAGAGAGTCTGGACAGTGGGGAGGCTCAGCCGCTGATCATCGGAGGCGCGGG CACATGGCAGGGATGAGGGAAGAGCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAAC TAGACAATCACGTGGCTGGCT
ESTD-PAI1	100 A G	---	---	

ESTD-PAR	120	A	---	---	CTCTTCAGGAACCAACAGTCTTCTTACCAAAACACGACTTATTTGCTGTCGAGAGGTACAACCCGTAGA
ESTD-Per/RDS	74	A	G	---	ACTTCTTCTTAACGTAAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT
EST68308	5	29	C	T	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACTTTCTGTGTTCTAGAACGTTTTCTAG
EST54045	6	39	A	G	GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCC
					ACCTACAGACGTCGCTGGATGGTGTGTCACACCCCGAGGAATCTGAGAGCGAGACAGGGCTGGCTG
					CTGGAGAA/GJGAGCGTGCCGGAGACCTGGAAAGGCT
					GGAAGAGATTTAAGAAAGCTTGATTGGA/CJTAATCTGGTCTTTGAGTGTGGAAGATTCATGTC
					TCTGCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
					GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
					GGAATATTAAAAATATTTAAAAATACCTCCATTTTGCCTT/GJTCCTTTTAGTGAAGATGATACCTGC
					AAAAGACATGGCTAAAGTTATGATTGTCTATGTTGGCAATTTGTCTTACAAAAATCGGATGGGAAA
					TCTGTTAAGTAAGTACTGTTTTGCCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD-PXMP1	88	A	G	---	ATGAAACATGGTCTTTAAATTTATGATATGTTGTTATAGCTATCTTAAAAGGGCTTCTTTTTTTA
					ATGCAGAAAAGAGGGGAAA/A/GJGAGCGAGCTGTGGTGACAAAGGTGTTTTCTCAAGGCTCATAC
					AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTTAATCTT
					CCCGAGGAATCTGAGAGCGAGCGAGGGCTGGCTGTGGAGAAGAGCGTGCCTGGAGACCTGGAAAG
					CTTTCTGGAGAGTGTGAAGAAAGCTGGCAAGGGCAACAGGTGGAAGCCGAGGGCGCAGACGCAGG
					CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT
ESTD-RDS	127	A	---	---	CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-s14544	94	G	T	---	TTGGGAAGTTAGAGCCTATATTAATTAACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAAAA
EST52908	0	45	A	C	TATCCCAAAGTTGAAATGCTCAGTTCG/CJCTGTGGGTTAGATGCAGGATTTATATGATCCGTTA
					ACCTCT
					ATCACAGGTCCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/CJTGCTGGTCTGCAAGCCCTT
					TGGCAATGTGAGATTTGATG
					AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATG/CJTGCTCAG
EST19590	55	C	T	---	GATGCCGGAATAATGAC
EST76136	39	C	T	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACC/CJTGCTGTCATACCTTTATCTATAGCCTT
					CCCCTAGGCTCT
					TGAAACACCTGTGTCCGGAGCCAGGTGTGTTCTCTCTGGAGCCTGAGGAGTTTGTGTCTGTG
					CAGTCCCGCGGCCACCTGCTGGTTGAGCCCTGGACATACACCTTCACTCTTGGCCCGGAGAAGAC
ESTD-SPTB	176	C	T	---	ATTTACCCACCTGGCCATGTCCCTGGCTGTTGTGCA/CJTGCTGTGTGAAGACCCCAACCCCTGC
					CTCCCCCAACCAAGCCAGTTTCTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C	---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCAATTCATCAGGGCCATCAGTTCATTGAGCTC CCATGACTGGGATGCTAAGTCAGCACTGAGTTCATTCTTAATAGACTTGGGACAGGATCA ATTCCTCTCACCTAGAACGTTTGTACAACTTTCTCCAGATGGATGGATTATGATGGGGG GAGAAAGCAATTTTAATAGGACCCATGAGACATCA
ESTD- THR	125 A C	---	---	---	TGCGGCTTTCTCGGAGGGTAGACTTCTACTTGGCTGTGATTCCAAGAGAAAGATCCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGCCAGTCTCAATCACACAGGATC A C TTCAT CCACACTGGATTGGCCAAACAAGTCTGAGTCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD-TYR	122 G T	---	---	---	TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTGTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTTCAG G TATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAA CATGGGTGTTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGATGACA
ESTD- TYRP1	222 A C	---	---	---	AGTAGTGGATGAAGCTAACCGCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTTACCTTTATTACCTTCTTCT AATACAAGCATATGTTAG A C ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	---	AGTAGTGGATGAAGCTAACCGCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTTACCTTTATTACCTTCTTCT AATACAAGCATATGTTAG A C ATTAAGTTCTAGGCATACTT
ESTD- VB12	148 C T	---	---	---	TCCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA C T CAGACTGAGAACCCACCGTTATATGTTACTGTTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T	---	---	---	TCCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAAGGTCACAGACAGGAAACACAGTG ACTCTGAGATGTCA C T CAGACTGAGAACCCACCGTTATATGTTACTGTTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	---	TCCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC A G TGGATGCTGGAATCACCAGAGCCCAAGACACAAAGGTCACAGACAGGAAACACCA GTGACTCTGAGATGTCACCACTGAGAACCCCGTTATATGTTACTGTTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGAGAAACAGGACAGCCACAGTGCGCGGGATGCGCGGGAGTTC TGGTTGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCCTTGCGGTGCGATGCGCTAAACCTTTGT TTCTGGCCAAAGGAGGGCGGGTGCCATGCTGAGATGATGCGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAAAGAGTTGATTAGTGAAGGAGAGATGGACCTACCTTCCACACTGTCTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGTCAAGCCTCAGCACAGATGCTGTTCTAAGGATGACGTGCTGTTTACAA CATCTCCTCGATGAAGAGACAGAGAGTTATTTATCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTAAGTGTGTAACAACAAGAGAAAACCACTGCAGATACCAGTCGTTGTTGGTGGGA AGGAGTCCCCAGTCCCAGGTGACACTGGACAAGAAAGAGGCCATCCAAAGG
ESTD- TNFAb	152 A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG CAATAGTTTGGGGGATGAGGACGGGTTGAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTCAGGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATG CTGTGTGCCCAACTTCCAAATCCCGCCCGCGGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG CAATAGTTTGGGGGATGAGGACGGGTTGAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCAACTTCCAAATCCCGCCCGCGGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCCACTACCCCTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGGCGAGTACGGGCTGCAGGCATACACTAGAGTGAAGTGAAGTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTGCCAGCCCCAGGGACAGAGCTGATCCTTGAATCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGCGCTGCTTATCAGCCTCCAGCCAGAGCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGGGCCCCATGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGATCTCTCTC CCTCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGGAGGAGGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGCTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGACGAGGAGGACCTGTCCCAAGCAGATGATTTACCATTTCCACAGTGGT CCCAGTTTAAACATTTCTATGAGCCAGGAGAAAGATACGTTATCTCTGCAAGCGCGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60	C T	---		AGACCTCAGTTTCCTCTCTGTAAGGGAAGTTTGTTCTGGATCTCCATGGGCCAGC/C/TAAGCA CTGGTCCCTGTGAGTCTGATCATAGAGAGATGGACAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
EST39852 8	106	C G	---		CGGCTTCCTCCAGGTATTGTCAGAAAGGCCGAGATGACCTCTATGTCAGATGCATTCCATAAG GCATTTCTGAGGTGAGTACACCTTCCCACCTCTTAC/C/G/GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGAGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	A G	---		ACCTGGTGTGCTGGTGGTGAACCTGCTCTCTTGGCATTGCCGCCCTCCTGGGGCCCGTGG TCCTCCTGGTGTGTTGGGTAGTCTGGAGTCAACGGTGTCTCTT/G/GTGAAGCTGGTGTGATGGCA ACCCTGGGAACGATGGTCCCGCAGGTGCGATGGTCAACCCGGACACAAGGGAGAGCGGGTTACCC TGGCAATAT
EST36027 2	120	A C	---		AGTGACTTCCAAGGAAATGGTACCCAACTTGCTTCCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACTACCACCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG/C/AAACCTGAAAA AGGCTGTCAATCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTAGTGGCTGCTCTAAAAGACAAATGAATGGGGAAAGACAA
ESTD- COL2A1cc	112	A G	---		AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGCTCACTTTC/C/G/GGGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCCGTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAATACTGCGCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97	C T	---		TGAGAGAACACCTAGTCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGAOCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAAAC/C/TTGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAAATTTTATTTGACCAAAACACTATCATGGAACA GCATT
ESTD- CPT2	150	A G	---		GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAGGCCCTTGAAGACATGTTTGACCTTAGAA GGCAATCCATCAAAAGTTAAGTTTCTGGGCAGATGAAGAGCTACCATCTCCTCATCATGAAAAAC TGGGAGGCCGGGCA/TAGTGTCTCATGCCGTGTAATCCAGCATTTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCACAT
EST12274 0	135	A G	---		CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCCTTACCAAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACCTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTG/ A/GTGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCCACCATGGAGGATACTATAAAGTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91	G	---		ATGCTAAGGGGATCGGACATGAAGGACCCCTGTGAGCCGATGTCCTATCTCCAGCGGCCCTGTCAATC CAGCTCACTCAATGAGGGCAGTCAGGCCOAGGCAGTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

ESTD- SSA1	111	C T	---	---	TTCACATTGTGGATTGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCAATTTGTCCAAG TTTGCTTTGGCTGCCTGTGCTGTGGGATATTTGAAGAGAT/C/TJTTGCCAGTCCAATGTCTCTAGA GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTCTGTGA
ESTD- RVRI	109	A G	---	---	CTTCGTACGGGAGGTCACGTCCTCCGCCCTCTTTCATGGACATATGGATGAGTGTGACCATTTCCOC CTGCTGACAGTGTGATGACACGCGAGACTTGTCTACTATGAG/C/GJGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGAGTGGAGCCACCTGCGCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCAOCCGAGG
ESTD-WT1	70	A G	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCGCTGCAGGATGTG CG/C/GJCGTGTGCTGGAGTAGCCCGGACTTGTACGGTCGGCATCTGAGACCAAGTGAAGAACGCCOC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST4438 7	100	C	---	---	GATAAGTACACTGAGGCCGCCAGGAGGTTATTGCCTAGTAGCCCCAACTGTGCTGCACGCTTAAACCTCT GCACCAATGGCTCCAAAGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCCC AGCCCGAGTCCGGCCGGTGGCTGGTCCCAACAGAGGAGGCCCTGGAGGAGGAGACAGAGATGGGC TGGATGAG
ESTD- PBDA	103	A G	---	---	GCAGCCAGGAGCGCTGCACCATGCCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGA/C/TJG TCCTGCTCGACCTAAGCGGAGCGCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122	A G	---	---	CCTTCTATGCCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/C/GJCTCTACCCGAGCTTGTCTCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAGCCTCGTACC
ESTD- CTLA-4	48	A G	---	---	TGCAAAACACAAAAATCTTCTCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCCTTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/C/GJTCAGATCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTACITATGAATATTAIGATACCTTAGCTTAG
ESTD- ACE	96	C T	---	---	ATGGCTTGCCTTGGATTTCAGCGGCAAGGCTCAGCTGAACCTGGCT/C/GJCCAGGACCTGGCCCTG CACTCTCCTGTTTTCTTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCTCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
EST54419 8	88	A G	---	---	GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TJGTCTCCCTGGCTCGGGGGCCCAACCCCGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAAATCGGCTGC CTTCGCTTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC/C/GJATCCTGGGAGATGTTATTTGGGTTAGCGTGGTGTGTTGTCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGAGTAAACCTTGGATTGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACAAACCATAGCCTAGJTTCGTAGCCATATTAATTTGGTTTGGCCTTAC ATTATTACTCCTTGGCATTTCAGAAAGCATTGCCAGCTCTCCAACTCCATCCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTACTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCGTGGGAGCGGCCCTAGCCGGGCGCTGCTGGCGTGGCGTGGCGCACCC GTGGAGGCAACCTGCTGGTCACTGGTGGCCATCGGCCTGAGACTCCGAGACTCCAGAACCATGACCAA CGTTCGTGACTTCGCTGGCCGCGAGCCGACCTGGTGATGGGACTCCTGGTGGTGGCGCCGCCGGCGCA CCTGGCGC
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCTCACCTCTGCTGCCCTTGGTTCAGJAGCCCTCATCTCTTTTA CAGGATCCGCCACACGATCCCACTGATCTGGCTTAGGCTCTCTCCAACTCCATCTTCAAAAAG GCTGCCACTGTGATCTCCCAAAGGATCTGATCTGCTACCATCTTGGCTCAAGCC
WI-801c	58 G T ---	---	ATGGAAACATTTCTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGGTGGGGCTGTGC ATCTGTGTATGTAGTTACATGGGCACATATACGCTCATGTTTTGTCTCAGCCCAACCAGAGAGTTAA CATCTGCCACCTC
WI-801b	58 G T ---	---	ATGGAAACATTTCTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGGTGGGGCTGTGC ATCTGTGTATGTAGTTACATGGGCACATATACGCTCATGTTTTGTCTCAGCCCAACCAGAGAGTTAA CATCTGCCACCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATATTACATTAGTCTCATTATTCTGAAATATTAT TTTTTACA/JGTACCCCTTTGATTTTGTATTGATTCATTTGIAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATGCTATCACAAATGCTAAATACITTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTGCTTTAIGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACTCTGTTGGCTTCATTATAGTAAAGGAGATGTAATTGCTGATGAGCCTCT CAA[C/T]TTTAACTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTTAAAGAGGAGACAACCTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCCTCTCTCAAGAGACTTTTACATTTTAGAC AGG[C/G]AGCAGAAAGCAGCAAGGAGAAAGGAAGT

WI-2625	98 G A	---	---	---	GGG CAGTCTGGCTGTAGTGGTAGACAGCAGCTGAAGGATGGAGGAAGAGAGAAGAAACAGGCAGAA GCACTGGGTAGTTAACAGGCTTATTAGGA/GA/CAAAATTGATGATACCTCCCTGAGGACTCGCAG AAATTACGAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAG
WI-2924	54 G A	---	---	---	TCGTGTGCATATTTCCTCTTTGACTCTGACCTCCTAGTCTCTCTTATAGG/GA/JACCCTGTGATT ACACTAGGCCCTACCTGGATTATTTAGAACATC
WI-2939	72 G T	---	---	---	CCATTGTGAGGTTGGGTGGGTCACCTTGTCATTCCTCGCAGCTCAACAAAGTGGCTTGTCTCAGTGC CTTTG/JCAAGACCTCCCTCAACAAGAATGTCTTCCATGCTCCCGTGTCTTTGAAAATTGACT TTATCCTGAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A	---	---	---	CTTGCTACCATGTCATTTACAGCATACACCCCTCAGTGAATGCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGAGACGAG/GA/JCCACACAAGGCAATACCTTGAAGTGACTTGGA GAATAAAGATTGTGGATGGATGAAGCAGAGAGAGATGCTAAAAGTGA
WI-3473	101 A G	---	---	---	GGAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTGGCCCTAGGGA/GA/JTAGAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAA/A/GJTGAGGGCTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796b	29 A G	---	---	---	ACACACTTTTCTGTATGCTCTTCATCAA/A/GJTGAGGGCTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796	29 A G	---	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAGATGGGGTGAGT AGTCACATTAGGTATTTCCAAATAA/C/JTAAAAATGCCCTCGAAAAATATCTCTCCCATGTGCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T	---	---	---	GCTGAGCTTTGTGGCAGAGCCAGGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC/C/JGGGTAACTGAGAGTGGTTTTTCACACCCAAA
WI-1959b	87 C T	---	---	---	GTTGTGCCCTGTAGCAGACACAGAGGCA/GA/JAGAGGAAAAAGCCTTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G	---	---	---	CTTGAGTATCGTGGATTTTGGTATACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGACAAATTGATCTGTTTCTACAAATTACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAA/C/JGACAGTTTTTAATTGAGTGAAATTACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGGCTATAATAGC
WI-1980b	140 C T	---	---	---	

WI-2015b	190	A G	---			TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACACAGACTAT GTGTGAATCGTCTATTAGGGTTTGCATATAAAGTCTACATGGTGCCTTTTCCAACTT[AG]CATATACTT CTAATACCATAGAG
WI-754b	49	C T	---			GAAGGCACAGGAGAGAGATGGCTGTCATCTACCAGCCAGGGAGAGAGAGC[CT]ACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTACTTTAGA
WI-754	22	T C	---			GAAGGCACAGGAGAGAGATGGCT[CT]GTCATCTACCAGCCAGGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTACTTTAGA
WIR-1b	56	A G	---			AGGCAATCAGACCTACAGAGAGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGGCGCTG GAGGGTGATGCCTCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56	A G	---			AGGCAATCAGACCTACAGAGAGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGGCGCTG GAGGGTGATGCCTCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72	A G	---			TAATTTAAATGGGCCAATAACACAGTACTTATCTCAGAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[AG]TCTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAAACAAATAAGCA AAGCTGGTGCTGAGATAAGA
WIR-3a	69	A T	---			TAATTTAAATGGGCCAATAACACAGTACTTATCTCAGAGCATTTCTCTAAAGGCTAAATAAGAA GAAT[GT]TATCTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAAACAAATAAGCA AAGCTGGTGCTGAGATAAGA
WIR-4	47	T	---			GAGCCTTTCTAAATTAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209	C	---			CGGGACAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCCCTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196	C	---			CGGGACAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCCCTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194	C	---			CGGGACAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCCCTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-5a	37 A	G	---	TAACCCCTGAAACTTTGTCTTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTTGGGCGAG
WIR-6	63 A	C	---	TTGCGTACTATTTC/TJAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C	T	---	GGCGTCTATGACTATCTCTGGTCAATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46 C	T	---	AAACAGAAAAATAGAGGTTATAAGGATGAACTAAAGTTGTGAGAAGAGGATGATG[C/G]CTGAAG AAAGAACTACTCTCTTTTGACCAATAATACAAATGGGAAACACTGGAAACCATGGCTTGATTACT GACAAC
WIR-2	56 C	G	---	TGTCCTTGCTTATGCCTGCCCTTTTCGCTTGGCAGGATGATGCTGCTATTAGTATTTCACAAGAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTGTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAATGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93 G	A	---	GGTCATTTCTTTTATCTGTCAGGCGCCAGCTCTGACTTATCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTCTTCCACCATGATGATTATACCAATAATACAGTTCCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	CCTATATTCA AGTTTGGAAA
WI-18612	37 A	G	TGC	CACACTGTTACACACCTATATTCAAGTTTGGAAATGG[A/G]TATTTCGAAGCAGCAATACAAAAGTA TTCATGAAGAAATGCATAATCTCTGAAAAATTAAGAAACATCCCT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGACAA GTGCAACA	TTAAAAATCACTAGGGCTCACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGOC ACAGGAATCAGCAGCCTGA/C/TJTGTCACCTTGTCACCAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTTAA CTGCACTTTT GC	CGATTGACAACTTTTATTTTCAACCTTAGGTAAACAGTCCAAAATCAGTGTAGATTGGCGAAAACT AGGCAAAAAC/C/JAGCAAAAAGTGAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTTCCTCTACT
WI-18680	75	T C	AGCATCTGGA	CCTCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGA/T/CJGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACACACCAAGGGCAGGTGGGCTTGAAGGAGCC CTTGAGGAAACACAGGGTCTCCGAGGGGTAC/CJCCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGCAACCTTGTTTAAATGCAAAAC/CJACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTCGTGGGTG GGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTAAATCCCTATTAGGATATGAAAGGATTGAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGTCTGCGGGTGGGGGTGCAAGT/CJGTGTCCTCTTC AGTGGTATTGGGAGC
WI-18533b	91	T C	---	---	GGGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAACTCCCGGAGATTTCTCTCTTTATTT TATATTTTCATTTTTCATCCTAA/T/CJTACTGAAGCCATTTTCTTTGGTTAACTTTTGA
WI-18533a	59	T G	---	---	GGGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAACTCCCGGAGATTTCT/GJCTTTA TTTTATATTTTCATTTTTCATCCTAAATTTACTGAAGCCATTTTCTTTGGTTAACTTTTGA
D11734	83	A C	TCATCTGATAC CTTGTTTCAGAT TTC	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCACTGATA CCTGTTCAGATTTC/CJAAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGACGCTGCAGACACAGAGCACAGCTCATGGGCAACATCAGTGGGCCCCAGAGAG AGCTGTCCGCCAGTGATCATTAGGGGTCTTTTATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT/TJGGCCCTGGCCTGAAAGTGGCCCCATCATACCCACTGTT CT
EST10030	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGGTGTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT/T/CJTATCCATACCACCCTGCTGATTG
EST10052	24	G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/GA/JAAGTCTAAGATTGAGGTCCACATCTGTGAGGGCTTC CTGTTGAGTCATAACCTGGTGGGAAGTCAATCATGTGGCAAGAGAGAGGGGCTACAGAGCAAGAGGAA A

EST110605 2	118 C G ---			CTTGGCGTAATCACAGTTCTGTATTATACAAAAACTTTGTTTTCTCTGACAAAACGTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTAAATTTGTGGAGATGCCCATGTG/GJTTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST111048 0	61 T G TAATCT	CTCTCAAGTAG ATAAGAGGCA	GCTAAATTTTC AGAAAGAATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAAATCTTTCTGAAAATTTAGCTTATGAATCATTACACTGCAACACAGAGAAGGAGCAC TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG/GJ/GGAAATGAAGGCAATATCAGATAAA TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCAAGTAGATTCTTTTGGACGAAGAAAAATCCT TCTGTGATTTCAGCTTTACGGCTTTCTCTCATCTGCTGGT/GJ/TTTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
EST111349 9	101 G T ---		---	GAATCTGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAGCATCCACCTACTTTGGAG CCCT/GJAGGAGTTTTAGAGAAAGCTGGAGCCGAGAGCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGAA
WI- 16632a	71 A G TGGAGCCCT	CCAACCTACTT CTAAAAACTCC	TCCAGCTTTCT CTAAAAACTCC T	CCAGGAATAAAAGAAAAAGAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA/GJ/GACTATTTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA CTTGCCATTATTTTGTGCATGTTGTTCTTAAAGGCTTGTAAGAGATAACTTGGAAATGTGGGAAC ACATAGATCCCAGAG/GJ/ATTAAAGGGGCTGGAAAAAGTAGCCTTAAGAC
EST111772 6	74 A G ---		---	AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC/GJ/AGGTATACATGAAGTAAAAATTC ATGAAGTAAAAATTCATTATACCAAAAAGCCTCCACAGAACTTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST111795 3	82 G A ---	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC	GCCTAGTAATTCAAAAAGGAACATGTTGTATAATAACACTCAGTACAAAGTCTGT/GJ/ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC GTGAAAAATTTTTTATCTGTACGCTTTCC/GJ/ATTATATTTATCTTGCTTGTATTCAGCACCC CACCGATTTCAGGCAGTGTCTTCTAAACTGTGCCCTGTGAGCTGTAAAAAGTCTTCT
WI-16644 42 G A TAC		TTGTATAATA ACACTCAGTA	GGCTGGTCACT TCCTGGAT	CCCTTAGCAAAATGACTTGGAGTTGTGTCCTCAATACCAAGTTACATACTGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT/GJ/GGAAACCCAGACGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12005 9	56 A G CAAAGTCTGT		---	ATCTTGAGGTTTCTGGCCCTGTCAG/GJ/AGGTGACATCTTTTACTTACCACAGGTGAGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTTCAGACTTTTAAAGGGCTTCTTATCAGCTCAATAAA
EST12055 9	32 T C ---		---	
EST12492 1b	95 A G ---		---	
EST12492 4	25 A G ---		---	

EST12502 2	52 C G			ATAACTAGGGAGAAAAACCAACTGGAGGCAAGTCCACAGGTACACTTGTCA/C/G/CAGGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTCAGGGGGAAATGACCATTTTAAAGGGCCATGTG GTGCTCGAGGAGTTAGAGG
EST12619 8	105 T C			CCAGAGAAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTAATCCCAAATGACAGTGTGCTGAGAT/C/GATGCATGTGGCAGACGAG
EST12620 0	67 A G			TTTTCTCTCTCTCAATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC/A /GJTGAGAAATACAATATTGAAGAAGAGTCACTGCCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A			TGGGGTTCTCCAGGATCCAG/C/A/CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGATGGGAATCCCATGTTGCTTTGGGTACTCCATCAGGTCATTGG
EST12941 8	23 T A			TCTCAGCTTCCACCTGACCTGCA/T/A/CAACAGCCAGTTATTTACACAGAAATTTGTTTGGGTTTCA ATGTAGTGTATTAGCTTTAATACACTGCACTTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTTAAAAACAACAC/A/GJCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T			ATTTTTGTTTTCTTAATGAAGCATAATAAACAGTTAAAATTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTTAATCAGTCTTCTAGGGCCACA/C/JGGAGCAGAAGCAGCTTCCCACCCAAG CACCTCTGAAT
EST13117 6	66 A G			TGCTGTCTGCATCAGTCCTTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCAC/A /GJATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTGTCACATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T			TCTGCTTTAAAGATTCTCATAGCTGCTTAGGTTTGTCTTCC/C/JAGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTCAGGCGAGTCTCTCACTGTCCCATGAATAGCC AGTCTTATTCCACTCT
EST13226 6	74 T G			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATGAAATAGTCT GGCCATTT/GJGACTAACCAAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	COGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTACTGAACITACAACCAACTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC/GJATCTCTGTACAGGAGCCGGTACTGTCTTCAATCCTTTGCATGCGGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAAAACACTCCCATCAGTAGCAATACAAGTTATACATTTTAAACCAGATTTTCTCAGG CC/T/CJTTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCCTCTTGATATAACCA

EST13278 2a	51 A G	CITTCACCGAA CAATATTTTAG G	CATATCTTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAAGCTCCAAACCTTTTACCGGAACAATATTTTAGGAG/GJATTTGAAATTAT TTCTGTAGTTCTCACCACCACCAAGAAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAATATTTAGATAATACCTGTTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAAATCCACACATTTTCAGTCCAAAGAT/JAACCTTTCCTCAAATTTTCCATCTCCCATCAGA G
EST13290 9		CAATTTT TAGA AGTTTGGGTTT	AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAAATTTTAGAAGTTTGGGTTTCTT/JGCTGAAATTTCCATGAAGTGATTTTT TTTTCTGTGCTTAACCTTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGGGCTTTTITG
EST13518 2	45 C G		---	GAAACATCCTCCAGTAGATTGAGGTTAAATGATTGAGCATTTA/C/GJACITTTAAAAATTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	66 A G		---	CAGGTTGGTGATTTCTCAACTAGAGCTATTTGCCCCATCCCCACCCGCGAGTGTCTGGAGAC/J G/GTTTTGATTGTCAACAACCTGCGAGAGGTTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA/T/C/GCACACAAGGAATAAGGAGAGAGGTTCCGGTTAGTTGAGGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAATGGT
EST13785 0	101 C G		---	AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACAAATTTATAGCAGGTAAACCCAA CTGAAAGGAACAAGTAATGACTTCTTGAACAAA/C/GJTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G		---	CCTCAACCATCTGTAAACCCGAGCC/JGJGAGTGACCCGGGACTTGCTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G		---	CAATGGTGTCATGTGAACATAT/JGJACCTATTTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAAATGACCGAACACAGGAGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AAATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTAT/CJTTTTGAAGATCTTTTAAAAAT ATTTGACTTGTCCCTTCACACTATTTTAAATGT
EST14812 2	50 A G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTTAG TTAAATCCCAT TATGTACT	TTACACTTAGTACCAAGGATGCTTTCAGTGCAGCTTCTACATCTGAATA/JGJAGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGAGTTTGCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATACCCACCC ATACTGGTT	CGGGAACCA GTACCCGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGGTGAGTTGCGCGCTCTCCCTGCTGACCCAGTAAT TCACACAGACAATGGCGACCCACTTAAATAAATTTGCCCGTATCACCACCATCTGTT/JATTTCC GGTACTGTTTTCCCGTA

EST15420 6	109 C A ...	GAAGACAA AGACAACAGA G C GGA	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	TTTAAACCAAGACATTGTAGATGTCAGGACTCCGATCAATTTCTCTGCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTCTCATATAATCATATAGCCAAAGGACTC/AJGGAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GGTTTGCCAT G C CACAAGC	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	GTCAACGACACTTTTATTAAAGAGTGAAGAGACAAGACACAGAGGAG/CJAGCAGAGAAATAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTGA AAGGATTGAAAACATACCTAGATCATATAAAATTTGTGAAGTTTGGCATCACAAAGC/CJAJTTATAG GGAATAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATGCCTCCAAAGT CTCTCTCTCTAGACGTGGAATACACACGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGAG/CJGATGGAGGAACAGAAAGATAGAAGATTGGGGT GCTGATGAATTTGTGGG
WI-16739	57 G A	GGTTTGCCAT G C CACAAGC	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	AAAAATGTAAACCTAGAGTTGCCTCTTTTGTGTACATTTTCTGTGAGATGCTTTTACCTGAGAG/A/GJ CTAATAAGGATTGAACCAAGCAGTATTTTTTAAATGGCAAAAGTCCAGATGTAACCTGAGT CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTGAGGCAACATAGGAT/CJGTGA CAGCACCACTCGGACCAAGAGTGTCTGAAATCGTCACTAGCTGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST15948 2	58 T C ...	TCCTGAGATGT CTTTTACCTGA A A T C C T T A T T A	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	GGTTTGAAGACGACGCTTTATCTCACCTGCCACTGGGATTCATTTTGAGAGCTGTTTGTGACGCC TTTTCCAGAAAAGGCCGCTC/CJGGGTTTCTGAACCTCTATGGGCATTTTAGAAT CGTCTGAAGTTTCTTTTATCACAAGTCACATCAATCCCTCGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/CJTAAGAGCCATCCCTGCCCTCTCTTTGCT ATCCAGCTGTGAAGGACAGGAG/CJGTAAACACAGTCCATTTATAAGGGGTGTGCACATCCCA GGGCTCCAAATAATGCAACATTTGTTCACTCGTCCATGCTGTGATAGTTTCATAGTAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16088 8	89 G C ...	GGTTTGCCAT G C CACAAGC	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	TTCTTTAAATAACCCACAGACCCCATGACACTTCCAAATTTACAGACAAAAAAGTATTGTCAG CTGGTTCTCTCAGGGA/JGTTGGCCCCGAAGCTGGCTCAGTTACCTCCAGGACCTCAGTC ATGGTATAACAAAAATCAGTTCAGGTTTTTTCTGAACAAATGATCCTTTGGCTTTCCCGTGGCATG CTCCTAAAAACAACCTAAAAACAACCCCTCTAGCTCTAATCAGTCACTAAGATAT/CJGAGTGGCAAGT CTTTTACA
EST16100 1	24 C G ...	GGTTTGCCAT G C CACAAGC	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	ATGGTATAACAAAAATCAGTTCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTTAAACAACCTAAAAACAACCCCTCTACGCTCTAATCAGTCACTAAGATATCGAGTGGCAAGT CTTTTACA
EST16104 9a	83 A G ...	GGTTTGCCAT G C CACAAGC	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	ATGGTATAACAAAAATCAGTTCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTTAAACAACCTAAAAACAACCCCTCTACGCTCTAATCAGTCACTAAGATATCGAGTGGCAAGT CTTTTACA
EST16118 0b	119 T C ...	GGTTTGCCAT G C CACAAGC	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	ATGGTATAACAAAAATCAGTTCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTTAAACAACCTAAAAACAACCCCTCTACGCTCTAATCAGTCACTAAGATATCGAGTGGCAAGT CTTTTACA
EST16118 0a	32 C G ...	GGTTTGCCAT G C CACAAGC	GAATAGCTGA AACAGAGATA TTATTCCTC GATAGTTGATG TTCATTATTCC CTATAA	ATGGTATAACAAAAATCAGTTCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTTAAACAACCTAAAAACAACCCCTCTACGCTCTAATCAGTCACTAAGATATCGAGTGGCAAGT CTTTTACA

EST16151 2	53 C T ---			AGCCAATTCAACGAACTCTATCAAAACACACAAAAGGCCTAGAGGAGAGATT[C]/TAAATGAACGCT AAATAATTCAAGGCAATTTTGTATCTAAAGCATTTTGTCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGGTAGGGAAGATAGTAGTGTGCAAAATAAAATGGTAAACACAGCAG[G]/AAATGGAA TTATAGCTTCTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b	59 A G ---			GCAGTTAAACTGTGGTTCACAACGTAATTGTTCTTCATAAAGAAAGAAATATCTAGTTG[G]/GJTAG AGGAAGGCACGTCTCCCTGGCCCTCTTCGTTCAITATTTTATGTCACCTGTCCTAACGTTGGCCCGTGT GCAAGAGAICTTTTGAGA
EST16198 4a	28 G A ---			AACTTTAGGCTCTGGCTTTCAAAATCA[G]/ATACAGACAGATAAGAGCTTTAAAGTATTTTCGCATTT CCCCAGAGGAAAAGCTCAGCATCATATAAACACACATGGGTGCACATGCTCACGCACATGGTGTCTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCAACTCCTGAGTCACAGTTTCATTTGGGAGT[C]/CCCTGTGCAGCC CTTGCCAGTTTCCACGAGCAGGATACCTCAGTGTGATTTCAGACAGGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCAACTCCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGCAGGATACCTCAGTGTGATTTCAGACAGGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTGGCTGGAACCTGGGTGCACATGCACATCCTTGAACATATCATTTGGCAA AGGGAATGGGTATCAAAAATTTGCTTAAGGCCAAGCAGGAGGCCATTGTTGGGGT[A]/GJACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCCTGTGGCTGTCTCCTGTCTCCAGCTGCTGTCCCAGTGGCCACA[G]/JTGTTGTAGCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTCTGTCTCCACTCTCTCTCTCCGCCGTGGGCTCACCAACC TCTCTCCTCCTCAATC
WI-16824b	83 G A ---			GTCAACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G]/JCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGGA GCCTTCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGTGTGCTG	TTCTTCATAAG	GTCAACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGT[C]/GTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTTATTCATTACAAA AATGGCTTCCAAACCATTAAAATGAACCTT[C]/GGAATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	GCTAATGGCA	TGTGAATTTGGG	TATAATCCATCCTCCAACACACACAAAATAAGCAGCTAATGGCAAT[G]/ACTAGTGGTCTTCCCAA TTACAAAGACCTGTGCTTCAAAATGTTTTCTCGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79	C T	GATACAGGCC ATATTTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCACTATAGGACTCTAGTTCTAGAAAGCCTTTGGGAGAACAGGCCACCCAG
WI-16882	99	A G	GAAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTTAGGTGGGAGAGACAATTCCTCCCTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTGACAGGCGGATTACCTGACATGTCATCTCCCT
WI-16888	70	G A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAAAT TAA	GTAGTAATGTTTCATCACTACCCGGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTCGATTAATTTGGTCAATTCAGAACATTCCTCAAT
WI-16905	75	C T	ACTGGCCTGT GTTGTTCA	GCTATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAACAGGAACCTTGGCCTGTG TTGTTCACTCCCACTGCCCTAGAGATAGACA
WI-16910	74	G A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTATATTCGCTATGACTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAAAGATGATCTGTTATAGAAACGATACCTTTCATTTGGGCTGAACCAAGTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAATACTACCACCTTCTCTGCTTACACAGAGCACTAAAATCTAGGAAATTTGAC TTTACTGCAGCCATTAAACACCAGCACCTGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTTCTCTGAAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGAGCJCCA CGGGCAATCACAATGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCJGACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACAATGAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATATTCJCTTAACCTTGGTCCAACTATTT AGTATAACTAATATGAGTTTATCTACTGATAACTTGAATGCCATTAAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATT CCAGCGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGTAAATAGTATTTCJACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAAGTTGTCAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTGCGCCCTCATCTGAGATTCJGTG TAGGACTGAAGGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46	G A	AAGCACCCAG AAGTACACTG	CACATTCCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTGAGTCCCTCATCTGAGATGTG TAGGACTGAAGGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCAACAGGA	AATAATACGGT	ATGTTTCAACAGGAAAGCCATGTCATGACATTCATAAACACCCGTATTATTAGAAGCTCATTTAAT
EST17127	74 C T	CACTCGGCAC	GGGAGGGCAGG	TGTTTAAATGCAGACAAAAATCAAGGCTAACTAAAGGCAGATCCAAATGACCCAGTGATCAACCTAGA
9b		AGACAGAGT	GGTG	GGTCCACAG
WI-17040	94 T C A	AATTCCTTAT	GGACTATGGCT	ATCCGCTCTCCAAACAGCATCCACAGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA
		CATCTCAAGCC	TATTCAGTGAT	CAGAGTCCTTGGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTCCCTAAGTAACAACCT
			G	CACGCGTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
				GAGAATTCCTTATCATCTCAAGCCAGTCATCACTGAATAGCCATAGTCCCGAGTCTCGTTTTCC
				AAATCTTCTCATATGT
				TTGTTTGTGTTTCTCTCTCTCCCAAGGGATTACGTATAGGTCCTTAACAACAGGGGATC
WI-17044	47 G T G	GCCAAAGGAT	GGGATCCCT	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTGCAGAAATGGCAGGAATCGAAT
		TAACGTATAG	TGTTTAAGA	CAAAAGAAAAGCAAGTG
				GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCTATAAATACTCTT/AIG
WI-17021	62 T A	TGGACTTGTCA	TGTAGAGTTAG	CAGCTGCCACTAATCTACAGGCACAGTAACACTTATACAGGAGCAGATGCCAAAGTGCCTGG
		GCCTATAACT	TGGCAGCTGC	GAGGTGCCAATAAATCAA
WI-17065	90 T C	CCAGAAAGGA	CCCAAGAGAC	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCGTAAATCAACATGTGCTGTTTCTACTCCGGTA
		AAAGCATAAA	AATGAAATCCT	CCAGAAAGGAAAAGCATAACTTT/CJAGGATTCATTGTCTCTGGGT
WI-17066	32 A C T	TGTACAGCCA	GAGATGTTGAA	TTCATAAGGTTGTACAGCCAAACATCACTGTTT/CJATTCAGAACATTTTCAACATCTCAAAAAAGA
		ACATCACTGTT	AATGTTCTGGA	AACTCGCACCCATTAGCAGTCATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
			A	
WI-17074	86 T G			TGCTGACTGTGATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCACTGTTCACAGCAT
WI-17104b	108 T C		---	AACTCTCTACACAGGCCIT/GCTACATAGGAGTATATTTGGCCAAAGACTCACCACTAGAAAGTGATT
				CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCCCTGATGCTTTGGAGCTTTCCCATTCATCCA
			---	AATCAGAAAGCAGTCAGTGGCCCGTGGTTCCAGACGGCTT/CJCTCTTTGTTAAGAAATTA
WI-17114a	37 T C	TTTCCATCAAG	TTGTATTATAA	AGGTTCCAAACAGATGTTCCATCAAGGACTTTGTTT/CJGTCCTTCACTCTGCTATTATAATAC
		GACTTTGTTTT	ATAGCAGAGTG	AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAGAAGACTGCAGCCACAATCAGAGTTACAT
			AAGAGAC	GGGA
			TTCTCAGAATC	
			CTGGAAGATAT	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC
WI-17150	76 T G	CTCTT	G	TTCTCTCTT/GCATATCTCCAGGATTCAGAAAGGCCCTCTTTGTCTGCTCTAATTT
				GAAATCGAATACGTCCATTCTTTGTAAATAACAATAACGTTT/JAGAGGCAAAAAGCAAGATTCGTG
				TAAACCAACATTGGAAAGGGGACACAGGGAGGGGCAGAGGGGAAAGGCCAGATTTTCAACGGTTT
WI-17163	43 A G	TAACGTT	TTTGGCCT	CCCTCCACATCTGCAGACAAA

EST20824 8	115 T	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTTATTATTCAAATCAGTCTCTGAAACTCAGGGATTGAGGTTTTTA AGGATAACTTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTCTGATTGTTGTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAAATGATGCCAGATGGGTACATCCTCAGAACTTCTCAGCCTTJAGTACACAAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTAGTGGGACCA
EST21904 b	128 G A GTG	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTC AGAAAGCAT	TGATTGTGGTCTGGAGCAGGTGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACCGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGAAAAACA GCCCCAC	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTTGCTAAGAGAAAGAT CTGTCTGGCATTTCTTTTTCGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAAATCTTAAATGTTTACAAGCACCATAATTTCTGCT ATTCTGCCATTTCJACCGCATCCTTCATGGTAGAGTATCACAAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAAACCA
EST22311 9c	92 T C ---		---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTTACTCTATTCJGTCAAAGCTGGGCAACTATCAGTACTATCTAATTTCAGAA CACITTCATCATCCAG
EST22311 9b	54 A G ---		---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCJAGCCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCAGTACTATCTAATTTCAGAA CACITTCATCATCCAG
EST22311 9a	41 T C GAGTTATAA	GGATTAGATC ATCTTTTATT	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATTCJACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCAGTACTATCTAATTTCAGAA CACITTCATCATCCAG
EST22319	19 A C ---		---	TCGAGGAGCTCTGAGGAGCJACACCAAGGGAGCTGTGTCCAGGGCCACCCGTGCAGGGCAAGTGTG GTCCAACTCCTTCCCTCCCTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTTCT TAAGCCTTTTTAACGT
EST22433 c	103 A G AA	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACCJAGTGTGTGATTAAGCTGAAGCTGAAATTT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G TTATCTGCACAT	AAATGGATCC TTATCTGCACAT	GCATGAATTTT AGTTTCAGTTT	TATCCATTTCAAGAAAAAAATGACTTAAAAATACAAATTTCTATCCCAGAAATGGATCCTTATCTG CACAJAGJCCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T	ATCCTTTTGT CTACCCCC	TTGCCGTGTA TTTGACTGTAA TG	GCCTTTTATGTCCTTTTAAACATCAAAATGTTTATAACACACACTTGATCCTTTTGTCTACCCCCA ATTC/CATTAACAGTCAAAATTACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCAATTTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTAAATTTTATTAATCTTTGCCCTT/AJAGGTTTTGACAGTTTTGTGCTTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAAACATGCAAGTTTCAATTTACATTTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCAGCTCTCCCA AGTGACACACTAGGCAATGTAAAGCTCCAGAGGCAG/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCAGTG
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAAA	GCCTTTGCCTA AGATTAAATAGT AACTACT	AAAGGCTGTTAGTTTGTGTTTTTGTCTT/GJATTGATGGGATTTAAAGTGCAATATAACTGAAG GCAAAAGTCCAAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	CTGACACGTCCTGTGTGGGGGTCCATGTGGCGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTGCTCAGCTGGCCTTGGTCACTTTGTATTTCTGCTTGGTGAAA TACCATCAGCCTTCC
EST23733 9	31 T G T	GGCTGTTAGTT TTGTTTGTGTT TT	TGCACTTTAAA TCCCATCAAT	TTTTAACGAAATCTCACTACTGCAAAATGCAATTTGTTCCTAGCTAAATGAATGCAIT/CJAGAGATTTG CCTGCAAAATATAATTTAGATTTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCTAG TCTTTGATACAGGTAAACCAGTTTGTAAACATTTATCAGAACTTACATGATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJATATATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAAACCAGTTTGT/CJACATTTATCAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAATGATAGAACCCAA/C/JTAGGCGCAATTTACATTTGACGCGTCAATGC
WI-17470	83 A G	GTCCCGTCCG CCAG	CCAGTGACGAG GCGA	GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAAT/CJGATAGAACCCAACTAGGCGCAATTTACATTTGACGCGTCAATGC
WI-17519	55 T C A	GTGTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAAT/CJGATAGAACCCAACTAGGCGCAATTTACATTTGACGCGTCAATGC
EST25356 3b	95 C G	---	---	GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAATGATAGAACCCAA/C/JTAGGCGCAATTTACATTTGACGCGTCAATGC
EST25356 3a	26 A C	---	---	GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAATGATAGAACCCAA/C/JTAGGCGCAATTTACATTTGACGCGTCAATGC
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAAT/CJGATAGAACCCAACTAGGCGCAATTTACATTTGACGCGTCAATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT CAATTGATAA	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAAT/CJGATAGAACCCAACTAGGCGCAATTTACATTTGACGCGTCAATGC
WI-17596	86 A G C	ACTTCCTTGTG TAAACACTCC	CATTCCTTATAG CTAGAAATCGA CAATAT	GGGTGACGCTCCAGAAATGGAGAGACAGCCAAATTTGGGAGCAGATTTGGATCCAGCTTCAACAACT ACTACCAGTTATTGATAATGATAGAACCCAA/C/JTAGGCGCAATTTACATTTGACGCGTCAATGC

WI-17623	46 T C ---	---	TGTTGGTTTAAATTTCCCATATAAATTAATGGTGGGCACATTT/CIGCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAAATCTTTTGCCTGACTTGGAGTTTTTGGT
EST26419 1b	46 T C ---	---	ATTTACATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/T/C/GGGCAGTCCAAAATTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A AG	CAAGAAGTTTG GACTGCC	ATTTACATACAGAGATACAAAGGCAACTATGTGCAG/C/A/AACAATCTGATGGGCAGTCCAAAATTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 G C ---	---	TCAGCTTTAATTTAAGGGACATGTAAATAAAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/G/C/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGTCTGTTTCCATCTTGGCTTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---	---	TACTTCAGTTTAAGGCCAAATTCACACAGAGACTGTCTC/W/G/JGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---	---	CAAGGGATTTTATTTGTTCCCTAAAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGATT CTATAC'AAAACATTTCAATCAATCTCTCTCTC/T/JTTCACATGGGTACTCTTTTCATGTACACAT CATCGAAAAACAGACTGA
EST27504 0a	33 G A ATTT	GCTGGTGTGAT GCTTACTGTAAT G	TTTTGCACTTTGCAACAATTTAATAATTTATC/G/A/JCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAAGTCTTTTCAGTATTTCTGTTCACACATCTGTGTTAACAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTG	TTATGGAAATG GCTTATGTAAAC C	ATCTTAAAGGACCATTAGAAAAAGGCCAGTCACATTTCTTCTCCAGTCTTG/C/TJAGGTTACATAAG CCATTTCCATAAATTCATAGCCTTCTCTTAGAGTAACACACACTCTTGTITTAGGAATGTTT
EST27788 3	100 A G ---	---	ATTTTATTAGCGGTACAATTCCTCAAGGTGTAAGGGTGAAGGAAAGGCCGAGGAGGCAAAATACAT TATTGAGCTGAACAACATTTACATTCGAAGGAC/A/GJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCITGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCCTTAAAACTTTCTCTTCTGTTGGATCCAGTGACGTGGAAGTCATCAGAACCCAC/G/A/JGTACTT GGAGTACCTCTCTGCAACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC TTATCCATTT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACACAATC/G/A/JAAATG GATAAGGCCTCTTGACAAATTTCTGCCACCTCCGTTTAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---	---	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA/T/C/JAAAAGAAATGATCAATCTGTTGCCTCT AAGTCAATGGAATGAAGAGCTGTGTCAGGGGACACACCCACGCCGTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTCT TFAAA	TTTCTCGCATT TAATTTTATAC CA	CATTGGAGTAAAGGTTCTCTTTAAAT/TAATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACACAGACAGACAGATGAGTTTGTTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGOCCTOOC TGTC	TGGGTTGGCAG TGTC	AGAATTGGTCTAGTAATGTTTCAGGATTTCGGTGATGGGCCCTCCCTGTC/TG/JGGACACTGCCAACCC CACAGCTGGAGGGGCACCTAAGGCAGTCATTTTGTGATTAGA
WI-17730b	68 T C	TGAGCCTGGGGAGAAAGACACAGAGTGAAGTGCTATTAGTTACATCATACCAAGGTACATACTG TT/CJACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGGTACATA CTGTTACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAAGCATATTGTCACT/GAGCTAACTCCT CAAAACAACATACCCCTTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	CTTTAGAGGACACCCAGTCTGTTGGACTTAGGGCCTACCCTATTCCAGCAGGTGCC/NGJTTATT TCACTTGGTTACGTCGTGAAGGACCGTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTCTGCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAAGTGC TCATTCTCTG T	ATTTATTAGTATCTGCTGTTGGGGTGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAAGATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATAAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA/CJAGCTCAGTA TCTGGAATCAIGCTTCTG
EST30223 2	99 A G	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTAATAATTTCCAG/GGGATTTAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAGACCCAGA GTTTCAACATATAGGTAGG/CJATAACCCAGGCTCTACCTTCCCTTCCGTGAGAACCTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAG/GTACCC AGAGTTTCAACATATAGGTAGGATAACAGGCTCTACCTTCCCTTCCGTGAGAACCTCGTGGGAC AAGAGAAACAGGAAATATTGTGCTTTCTTG/GAGCCTGTTTCTTATACCCCAATATCAAGAATT GTTGTTGCTTCTATAATGTTACGCTCAAAATCTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCTCTTGTTCAAA
WI-17835	30 G A	TG	AAACAGGC	

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTACTTGTAATATCAGAGACTGAACATTTTCACTCTTTAGCAATGACA TCGGGTGTCCAGCAACA/C/TGGGGTGAATTTGGGGGAATCTTATCACAATATTCT
EST31968 8b	95 T G	---	---	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAACCTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCATTT T	TGTAAGAATCA GTGGCAGTT	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGTACTATAAGT GCATTTTJ/CJATAATGGGATTTTCTGCTTAACCTGCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103 C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTCCCCCTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTCCAGGCCCATTTGAAATAGCAAAAGGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	---	---	AAGGCTTCCAAAGCATTTCAAAGGCACCTTGGGTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCQ/JG JTCTGATTAGGGAGACCCCCAAGCCAGTAACAATATGGTCTTGCAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA TT	TTTCTACAAT TAATCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTT/C/GJAGACTGGGATTAATTTAGGAAATATTTACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC C	TGGCTTAGGT TCTACTTGATG T	AAACTGTCAATTCCTAAAGTCTGGGATGACTTTCCTT/GJATTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACCCAGCTGAATTAATGTTTCAATCT GTATCTGATGTAGTTAACCATGGCCTGTGATGATTATTTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAATTAATCTTGGTTAAATCTTTGCCAGCAAAAGCAAAATAT/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGGCAGCAA AGCAAATA	CGTGTGCTACT AATCACACAA A	CAGCAACCTTTTTTTGTTTATAGCCTACTTCTCAAAAATTGTTT/AJTTTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACCTACCA
WI-17866 EST33301 4c	43 A T	ACTTCTCAA ATTGTT	A	GAAAAAAGTCAAAATGTTCCCTTTATGGTGATGCCACCATGATTCCTTCACACAAGCATGATC AATCGCCACGAGA/GJA/ACTGGATGCCAAAGAGTAIGG
EST33301 4b	80 G A	---	---	GAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTCCTTCACACAAGCAT/GJA/ ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTAIGG
EST33460 1	63 G A	AGCGTGGTTTT CAATACTAAA CA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAAGGTGGTTTTCAATACTAAACA/GJA/JGTAAACAATGCAAAATATT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACITTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAAATGAACACIAGITACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACACAAATGA GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGAGAAAATGTGTGCCAAATCTCAAGTGTGAA TJAGJGATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATCTATGAAAAAAGAGCAGTAGTTTCAGC TTACAAATCACACAAGT
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACACTAGCG AGAACAACTA ATAAAATC	TGGGAAAACATAAGTTAACTCAAGAATAIATCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAAACCTTACCATCAAAACACTTC CAGTGCATCAA
EST34343 8	95 C A	GGACCATATG ATATATAACT TCTTAAAGC	---	GGTACACAAATTTAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCTAAAGC/CJTGGAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17982	98 C T	CTTAAAGC	CGTTCC	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTTATGATAAAACACCTCTCATTTGTA AAAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTATGTACJCTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17993	118 A C	---	---	CCCATCCAGAAACCCCAAGTGTGATGGTGAAGCAGCATGAAACAAACATCTCCAGGCGCTCGCAGT AGAGGCGAAGGGAACAG/AJGCTGCCCATGTGCCTGTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGAGACCGGGT
WI-17996	84 A G	GTAGAGCGGA AGGGAACAG	AGGCACATGGG CAGC	ATTCCTTTATAAAACACCCATGTCCCTAAAATGT/CJAJTTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-17136	33 C G	---	---	GCCACTGAAAAAAGGTGCTCTCC/AJGJGTTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATAGTTAATCA
WI-18041	24 A C	---	---	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGCGCTTCAAGCACAGCCCTGCCCCCA/AJGJCTTTGA GATTCAGAATCCAGAGGGTGTCTCAGTCCCTTGGTTAGGTGCTTCTGTGACATTTCCCTCTTG
EST35164 8a	57 A G	CACAGCCCTGC OOC	CCCTCTGGATT CTGAATCTCAA	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCT/CJTGGTTACACATCTT AGJACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGCTGATGCTCAGCAGCAGTGTGGC ATGGCCATCCATGCTTT
WI-18052b	67 A G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCT/CJTGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGCTGATGCTCAGCAGCAGTGTGGC ATGGCCATCCATGCTTT
WI-18052a	50 T C	ATC	CTCAGGCAGCT CTGCTGT	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAG/AJTGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTGGTAGCAACAGAGGTAATG
WI-18054	46 G A	GAGTAAAA	TTCCA	

WI-18084	54 G A A G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCCTGGGTAGCTGCTAAGCTGTATTTTCAGAG/AG/AAATGTCAC AATCATACCACCTGGGAGAAAGAGTAAGCACAGTCTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAOC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATCTTGATATGGGGTGGAAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C	AACCCACTAC TTACTCAGAT	AAAACATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/CJATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGAATTTCTGTACTCAGAAGCATTTTAGGTTCGAAAGGATATAA
WI-18080c	80 C T			TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCGTG TTTGACITTTAT/CJTCTTAAGTAAATGAAGCCAAATGCAATGTTAATCCTTCCTTTGGTGTAT
WI-18080b	65 G A			TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCC[C/ AJTGTGTGACITTTATCTCTTATGTAAATGAAGCCAAATGCAATGTTAATCCTTCCTTTGGTGTAT
WI-18080a	41 T C	GCAAAATCA ATATCAAAT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTGTAAATTAATACTACTATGCC CGTGTGTGACTTTTATCTCTTATGTAAATGAAGCCAAATGCAATGTTAATCCTTCCTTTGGTGTAT GTGGCATCCTATAAAGCAGCCATGTGTGTAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTTGTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTCTGCAGTCTAGC TTAGGAGAGGIGITGAA
WI-18086	63 G A			AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCT TTC[C/JT]TTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTAATGTAAGAAAGGGGTGAG TCAGT
WI-18115b	71 C T			AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCT TTC[C/JT]TTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T	TTAGTGTACCT TTGGTATTCCT TT	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCT TTC[C/JT]TTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTAATGTAAGAAAGGGGTGAG TCAGT
WI-18136	78 A G			TTTTGAGAAGCAGTCTGTAAAGGCAAGGATGCAATCAAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTG[C/J]TAAGACAATAAAGCAATTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115 A G	CCATCTTCCG GAAGCTC	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTCGAATCTGCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTATCCAAAGCAGCCATCTTTCCGGAAGCTC[J/G]TGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGGA
WI-18190b	26 G A			TGAAAAGAGTCGACAGCGGGACACT[G/A]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62	G A	---	---	TGAAGAAGTCGACAGCGGACACTGTCATAAGTGGAAACAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAATCCTGGGGA
WI-18181	100	A C	A A A T A T A C A A C A C T C C C T T C A G A T C	C G T T T A C C A T T T G T T A A G C T T T T G	G A C A G T G A A A C A C T T G A A A C A C A A A T A C A A C A A A C A C A T T A G G A C A A G A A A T G T G T A A A T C C A A T G T G T G A A A A T A T A T A C A A C A C T C C C T T C A G A T C [A/C] C A A A G C T T A C A A A A T G G T A A A A C G T A T G T G T C T T G A A C A T T C A T A C A A G C A T T C C T G A G T A C A A A C T A G G G G A C A G G T A T T C A C A A A A C A A A T A G A G C A G A G T T C C T G C C C T C [G/A] G T G T G C G G G G G A G A G A G G G A T T C A G C A T T T G G T G G A G T A T G T T A A T T C C C T C A A G T T A A T C C T T C
WI-18215	78	G A	A G C A G A G T T C C T G C C C T C	C C T C C C T C T C T O O O O C	C A T T T C C G A A A A T C T G A T A G T T A A A A T A T C C C G T C T G G T G T T G A T T G T G A T A C A C T T A A G T [A/G] A A C C C C T G A A A A C C T T A T T A T T T G A A A T T G A A G T T T T G C T C A G A A A C T G G C A G A A C T T T T C A C A T T C T G A C
WI-18232	60	T A	A A	C	T T T A A A A A T G C T T A G A T T T C C T C A G T A T T T A T C A A T A G T G T G T A A G C T G G A A A C T T G A G T T T G A G A T C A C A T A T [C] C T G T C T A C T A G T C T A T T C A C T T C T G T G G C A T T T C G G C A G A A G T G G C A A T A T C C C C A A A T G T T A A T C G T A A C A T A C T [G/A] G A A A G C T G T T A C A G T A G A A G T G T T A G C A A A A A T T G G A T G C C A C A A C T T A T C A C C A T T C C T T C A A G A A G T A G G G T C A G A A T G T T C T T G C C T A T A T C T G C A A A A G A T C G A A C A A G
WI-17892	76	T C	A C A A A T C G T A A C A	C A C A G A A G T G A A T A G A C T A G T G A G A C A G C T A A C A C T T C T A C T G T A A C A G C T T T C	G C A T C A G A C A T C A C C A C T C C T G A A A A A A C C T T C T A C A A G A A T T G A A A A G T T G C A G G A C C T A A T A C T G A A A T A G G A A A T A T G G A C T A T C T T C A A A C T G C A C A A A T G A T G C A T G A A T C [C/T] A C A T T T G A G A C C C G C A A C T C C G A G G T A C C T
WI-18266c	119	C T	---	---	G C A T C A G A C A T C A C C A C T C C T G A A A A A A C C T T C T A C A A G A A T T G A A A A G T T G C A G G A C C T A A T A C T G A A A T A G G A A A T A T G G A C T A T C T T C A A A C T G C A C A A A T G A T G C A T G A A T C C A C A T T [C/T] G A G A C C C G C A A C T C C G A G G T A C C T
WI-18266b	124	T C	---	---	G C A T C A G A C A T C A C C A C T C C T G A A A A A A C C T T C T A C A A G A A T T G A A A A G T T G C A G G A C C T A A T A C T G A A A T A G G A A A T A T G G A C T A T C T T C A A A C T G C A C A A A T G A T G C A T G A A T C C A C A T T [C/T] G A G A C C C G C A A C T C C G A G G T A C C T
WI-18266a	97	C T	A A A T A G G A A A T A T G G A C T A T C T T C A A A	T T C A T G C A T C A T T T G T G C A	G C A T C A G A C A T C A C C A C T C C T G A A A A A A C C T T C T A C A A G A A T T G A A A A G T T G C A G G A C C T A A T A C T G A A A T A G G A A A T A T G G A C T A T C T T C A A A [C/T] G C A C A A A T G A T G C A T G A A T C C A C A T T T G A G A C C C G C A A C T C C G A G G T A C C T
WI-18312	73	A G	A A A T T G T A T T T C A	G G A G A A A A G G G A G C A G A A G A	C T G A G C C T T T G G A T A T G T G G T T A G T G T C T A T C A T A A T T T T G G A A A G C T G C A G C T A T T G T T A T T T C A A A T [A/G] T A T C T C T G C T C C C T T T T C T C C T T T T C T G G A T T C T A T T C T G C A T G T T A T A A A C A T C T A C A G C T G C T T A G G C C A T C C T G T A A G A A A T C A G G A A T A A G A G C T G A G G A C A A G A G G G A [G] T A T G T A G G C A G T G A G T C A G G A C T A T G C A A A A C C A T A A A A T A A A G A A C A T A A T T T T T T G T T G A T T C A C A
WI-18330b	66	A G	---	---	

WI-18330a	49 G A A G A	TCCTGTAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAG[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85 T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGTTAGAATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGATT[C/T]CTCATTGAGGCCCTCCATAGGCTGCAACACATCAAAAGGCATTAC TGTAAGTCTGAGAGGAGCTGAG
WI-18327	104 G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGATTTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAGAGCAGTACCTC CCAAACAATGGTGAAACAGCTTTGCTTAGGCTAGTT[G/A]GCTGAGCCATTGATGCGGAGGCAGA GT
EST37624 6b	102 G A ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58 C T ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCAC[G/C]TGCTGA TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGGTTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89 C G GCATCAA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTCTACCGTCTGAGTGGCCCATGAAGCCAAAGCCCATTTCCAGACATTTCAGA TAATCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117 A G ---		---	TTTTATCTGGGTACAGTCTCTTCTTAATGGCCTGAAGGTCAATCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113 G A ---		---	TTTTATCTGGGTACAGTCTCTTCTTAATGGCCTGAAGGTCAATCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112 C T CCCTT	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTACAGTCTCTTCTTAATGGCCTGAAGGTCAATCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46 T C ---		---	TTTTATCTGGGTACAGTCTCTTCTTAATGGCCTGAAGGTCAATCTCTTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75 A G CTCTGCATTG	GCAAAAAGGA CTGATTATAA	GCTAAAGTCAG CTGATTATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATTTCCCATGTTATGTTACATGGCAAAAAGGACTC TGCATTG[G/A]G/ATTAAGTTTATTAAATCAGCTGACTTAGCATTTGGGAGATTATTTCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACCTGCACTCT GGGAAGC	TAATAAAAGCTGACCAATTGGTAAACTGTGCTGGACTGAGAGAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAATACATTCGT/G/GCTTCCAGAGTGCAGTGAATACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAGATCT	TCGTTAGGAC TTGGGGA	CCTGCACCTCCTAAAGATCTTTTC/TTCCCCCAAGTCTTACAGAATGGTATATCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTGCTCTGTTTTCAGCTTTGATTTTTTTGCTTGAGAACCTTG TCCTCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTCTGTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCCTCAGGAAGAACAATCCCATGTTTCTGTTTAA T/C/TTCTCTTATGTGTTATACCTTCCCTTTCTCTTTCTTTATACACATAGATTTTCTTAAATTCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTCTCCAGAGTGGTGCCTCACGCCGGGGCCCGCTGG AGTCCGGGGCCCGCCCTGCTCCGCCCTTC/C/GGCCACCATCCATTCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACCTGGG CATTTCAA	TTGCAAAAATG AAGGAAAAA	TATAGTAGGTACTTCTTGTGTCAGCAGGAATTTATTCAGTCTGAAGTGGGCATTTCAA/T/CJGCGTG GTATTTTTTCTTTTCAATTTTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T T A C A	AATGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTTACATA/T/CJAGATAGAAGATTAAAGACCAT CACTGAGGTACATAGCTCAGAGGCGAGATTAGATTGGACCCAGGCGATTGGTTCCAGCATATA
EST38707 9	75 A G ...		ATC	GGATCCTCACTCACCTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTCCCGJAGJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTCAGGAACACAGG ATCTTGCTTTCTGAAA
EST38759 2	86 A G G T G A T A T G G	TGCTCCCTGA GGTGATAGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTCACTAGAGGGGAGAATAACCTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATAGGJAGJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAATTTCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTAACCAAGAGAAAATCAATAGGAGAGGATTGGCT/T/ATTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCGAGCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCTAAGTGGTAC AAACAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCCTAGCCATGCTCTTTCACTTATGTGTTCATTCAACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T T G A C	CACGAGTAAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACTTTCTCCCAAGTTTGGGTGGTTCCATATTGTTATTGTTATTGTTA TTCAACACGAGTAAAGAAACTCATGAC/C/TTCTCTTGACTCGCTCTCTCCCAATCTCGAT ACCGACTGCACGTGG
EST38865 2	72 T C T G T G C A T G C	GCTGTAGAATT TGATGATG	GGAAGGACGG AGGACACAG	CCTTAATGGATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGCG ATGCT/CJCTGTGCTCTCCCTCCCAATGAGACATATGCGAGGCGAGGCAAGAGCATGCTGGA TTTGCTTATGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCITCAATAAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCTAGATCCTAAATTCJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTCCTCC TTATTCATGTCTATCTCACACATTCCTTTATTTATTTTATTTTCTCACTTTCTCAAAATATCGGATTGTGC TCATGAGAAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TGTCATCTCAC ACATTCCTTTAT TCTTTT	CGATATTTGAG AAAGTGA AAA CAA	TTATTCATGTCTATCTCACACATTCCTTTATTTTATTTTATTTTCTCACTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	GCACAGCATG GCTAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACTAACTAACTTTTCATTTTGTGGATTGCACAGCATGGCTAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAT
EST38909 5	47 A G	GTTGAGGGAA ACTTATAACCT	TGTTGTTTTGT GAAACAAGCG	AACTGAATGGCAGTGAACACACTACACATCAAACTTAGGGAAATGTGGTTAGTGTGTACGTTGAG GGAAACTTATAACCTCAC[A/G]CGCTTGTTTACAAACACACGACGACACAGAGATTTCCAACTC CAGCAATGACAGGGCTAGGG
EST38911 9	85 A G	TGAATTCCTTT GGTGGG	CACTGCAATCT CACCCC	TAAACATTTCCCATTTGAATTTCCCTTGGTGG[G/C]GGGGGGGGTGGATTGAGATTGACGTCTCAAGATAAA TATCAAAATATATCAAAACTTCAAAATTTGCTATGCACTTACACACTGACATGAGCCACAAACATTT CCTTTACAGGGGACTGTAC
EST38955 5	30 G C	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGACCCCTTGGTGACQ[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCCCTAAGTTCCGGGCTCTCCTCAGTCTGGATGGCTGTGGGAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGCAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCTGTGGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTATCATCACAAACGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCTAAAT CCCTATTATTCATGATATTTTCA[T/C]AGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	CCTTGTCTC AATTTTAAAC CCT	TAAGGGCTAAT TCCCTATATA AAAG	GGTTGTCTTTCATGATTTTCTCATTTTCTATCAGGTTTCTGGTCTTGTCTCAATTTTAAACATTT T/C]CTTTTATATAGGAATTAGCCCTTAAACTGTGGTACATGTGCCAAATTTTCTCCAGTT
WI-16403	69 T C	GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCITTAATGGCTACAGAAAGAGG[C/T]GGTTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCAATTTAGAGCAATAGGTGCCCTGAA
WI-16406	24 C T	AGG	AA	

EST39236 0b	57 C	TCATCTGAGA ATAAACCTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGTTTTCATCTGAGAAATAAACCTTCTGCTCTAAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G	CCTGAAACAG TGAATGCC	GCACAAATAA ACATAGTACCG AGAA	CAAAACAGACCTTTGGTTTGGCTCAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTTGTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTTACCCACAGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T	---	---	AGAAAAACATTCTGCTGATCAGAGGAAGATGTATGTAGAAAAATCAGAAATCGACTGAATTCCTAAA ATCTAT[T/C]ACACTGAGAGGAAAAATGAAAAAGAAAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST39371 9	86 A	CATTGGATT GGTGAGAGG	TGATTTGAGAC ATTTACACATT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTCAAAATGTCTCAAAATCAAAATGCTTCTTCTAAAGATT GACATTGCCCAACCTGC
WI-17177	23 A	---	---	ACAAAGTACATATCCCAACCAACC[A/G]TCCATCCCCACCTGTGOCCTATTCTTCTTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCAGAAAGCCCTCCCGTACTCTCTCCCTGGAA G
EST39428 8	31 C	GTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTCTGTTGCTCCCAACATTTTGATT[C/T]GGTGGCTTCAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGCGCTAGGTAATTTCTGTTGCCCTTTGGTCCACAGACACAATTAAGAGATCAGGCT GGCTGTGC
EST39430 2	45 A	GGCAGAGGAA TAACTGATGTT	CAGGGGTGCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAAGTATGTT[C/A/C]CAATAACCCCGACCCCTGA CCCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGCTCTGGG
EST39446 7b	117 C	CTACTGACAT AGGACTTCA	TCCTGGAAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAAGAAATAACAGAACTATTATAT ACGTAATACACTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A	AAAGATTCCT GTAGACATCT	CACTTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTGACACATTCTTGACCAAGCCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCCTTCAGAAATTGCAAGTGCAGGTTCAAGTCAAAACCAATTC CACAAAATGGGACTGCTGAAGAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA
WI-18387b	84 A	---	---	

WI-18387a	57	A	G	CCTTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTACCCCATACAGTITTTGTG
EST40601	78	A	G	CGTGGAACTT	TTCTTTGGAAGA	GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTTGTGAAGTAAATGIGCGATG
9	78	A	G	GAAACAC	AAGCGTC	GCTATGTAGACATAAGA
				AGTGATCAC		TCCCAGGATGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACAAAGAGGTGACTCGCGTGG
				ATCTTCAGGAT		ACCTGAAACACAGGACGCTTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGGT	GCACACCCTTC	TCCATTCAAGTGATCACATCTTCAGGATAGGTAG/ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC
					ACACTGTTA	AGCTGTGAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
				CATTCTGGTCT	AAAACCTGATTT	
				TTATTTTGGGA	GTAAAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA/C/TTGTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA
EST43091	28	C	T	CA	CTAC	CCTTTGAACATCAAAAGAAATACAAATATATTTTTCACAAATTTCTCATCACTGTAAATTC
WI-18420c	108	T	C	CA	AAATCTCAGC	AGAGACAACAAGAAGAATAAGGAAATGGGAAGAACAGAGAGTGAATTTAAAGCAAAATCTTGG
				AGGAAGTTTC	ATTGCTATAAG	TTCAAGATCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAAT/C/TCCTTATAGCAATGCTGAGAA
				GAATAAGGGA	CCAAGATTTC	TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	AA	TTAAATTTAC	AGAGACAACAAGAAGAATAAGGAAATGGGAAGAA/C/TTAGAGTGAATTTAAAGCAAAATCTT
					TC	GGATTCAAGATCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
WI-18425b	101	T	C	---	---	TTTCATAGGTACTTCATGGGA
				CACCTGTCT		AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCCAAGGAAGCCAAAGATCAGACACCTGTG
				AGACAGATTC		CTAGACAGATTCAATGCACACAACAACAGAGGGT/C/TTGGGGTACACGGCGGAGAGCCAAAGAC
WI-18425	81	A	C	A	TGTGTGA	TAGGGC
						AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCCAAGGAAGCCAAAGATCAGACACCTGTG
				CTTTGGTCT	CTCCCTGACT	AAATTGAGGTCCGGTGGAACTATAAAAGGAAAGGAAGAGTAATCAAGGGAGGCCAAAGTG
WI-18449	129	C	T	AAGTGGGACT	GTATCCAGA	GGAAAGCTGATTGCTGATCTAACGTGCTTCCAGTTCCTTTTGGCTCTAAGTGGGACTA/C/TTTC
						TGGATACAGTCAGGGGAG
WI-18457	120	T	C	---	---	ATCGCTTCAATTGAAGCTGCTTAATTTCTCAGTCAACTGGTGGCCCAAGACATTATTTTATTCCT
						AAATGTCCAAATATCTGCCTGATGCTGTGTTTGTGCACATTGGGGCCACAGT/C/AAATAGGCTAAA
						AGGAGTCCCACTGCT
WI-18462	39	A	G	AGAGTGA	AGATGTTTCT	GGTGTATAGTGTCTGTACACCACAAATGGCAGAGGTGA/ATAGAAACCATCTCAAGCCCTAAAA
						TATTTACCATACATCCCTCACAGCAAAAGTTTGTAACTCTCGGTTTAGGGACTCCATTGAG
WI-18476	60	C	T	GAGG	GCACGATGGGA	TGAGGAGCTGTGACAAGCTCCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGGCTGAGGCT
					GTGAOC	CACCTCCCATCGTGGCCCTGGCCGTCCCTCCACTCACCACACCTGGCCCACTCCACGTTGAGGT

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WI-18491	109	G A	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCTTGTATCC	CTAATGAGATGAATACATGGAAGGCGTTTAGCAGAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTATTATTATTAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCCITCACCC GCCC	AGCCCTCCACTCCACTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTTTTATAT GTGAGGGCC[C/T]GGGGGGTGAAGGTCAGAGA
WI-17675	103	T C	GGACATTTGG CATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGAAAGCAGCTAGAACTAAACATCTTACCAGGTGCTGAAGAAAGTGTCTCGTTTAAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTACTT[C/C]CCTGGTGGTCCCCATAGATTACCCAT TGCCCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT	GATTTCATATT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCCTGAATGTCAAAACAAAGAGATAAACTACATTGGGTTTTGG[G/T]AAGTCCCCGTGAATGATGAATCAAGAATCCTCAAGTGTCTTGCCACCCATTTAATACGTATT TTTGTAAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAACCATCTCCCCCTGACCCCGAGTCCATGGAAAAATTGTC TTCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTGGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCATTTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTACTACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[G/G]ATTCCAGGACCCATAACTCTGTTCTCACATCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTACTACAGTGGAGGCATTTTCTAGCTGTGTT[G/A]A TTTGGCTCCCTATAGATTTCAGGACCCATAACTCTGTTCTCACATCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAACTCAGTGTCTAATCTATCATCTCCAGATTTATCTGAAGTGGAAACCCCTCCGACCCCA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCTCAAA
EST51717 a	39	C T	---	---	GATCCAACTCAGTGTCTAATCTATCATCTCCAGATTTAT[C/T]GAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	C T	TGTCACTTTG GGGCC	GGCTGTGCCA GGCC	TTTCCAGGTTGACAGGTTTATTCACCCCTTCCATCCCCATGGCCACCCCGAGGAGGAGACAG GTGTGCTGGAGTCTGTGCATTTGGGGCC[C/T]GGCGTGGGCAGAGCCCACTGGGTTTACATTTCTGT GGGAGGTTGGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG	CATCTGGATAT CTTGTACATTT TT	AAACTGCAATAACAACAAAAACAGAAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAAATGTAC[A/G]AAAATGACAAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAAA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC ACATTAAGGGGAGATGGCC

[illegible]

[illegible]

TIGR- A003P30	117	C G	---	CCAAACCTCCT CAATCCTATAA TTAAA	---	ACAAAGTTCAGGAGAACCTTCCTTTGTTTAAATGCAGCTGTGCTCAGAACCCCTGTGATTCCTAGGA AACCATCTGGGTTTAGCCCAATTAGAAAATGCAGTTTAAAGCAGTGTCA/C/GJACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156	C T A	---	CCAAACCTCCT CAATCCTATAA TTAAA	---	GCTTGCTTTTATGTTAGTTTCGGGGGAAAGGAGGGGCTGACAAACCCAGACATCTGGACACCAGC AAGGGTCAGGGGAGGTTTGCAAACTTCTTGCTTGCTTAACAGTCTGTGATGTGACAAATAGCCA AACCTCCTCATTCCTATAA/C/TCTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97	A C	---	---	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGTAAAGTACAGGAAGATAAACCAAAATGAT TGAGTATGATAAGAAATTTGCATGGCGATT/CJAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004T44a	69	G A TGA	---	GGAGATAAA CCAAATGAT	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGTAAAGTACAGGAAGATAAACCAAAATGAT TGA/G/ATATGATAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004V08	60	T C	GGCATTCCTT	CAGGAAAAA CAGGATTCCTT	TCCTTCCAC AAAGGC	CCTACAATCCTATAATTTGCAAGGGTTGGGAAGGATGCAGGAACAGGCATTCCTTAT/CJGCC TTTTGTGGGAAGGATCAATTTGGGTGCATGCACCTTAGGGGACAAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAA
TIGR- A004V26	125	A G	---	---	---	TCTAGCTATAAGACCAGATTTTAATATTCTAGATATAGAAATTAACAGAAATTAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA/VGJAAGGT TTCAGTTTATAAATGCTTAAATAGTGTATCTATTGCTTAAATAGTGTATCTATTGG
TIGR- A004V28 a	29	A G	CGATCTC	TGTTGTGGGTG CGATCTC	CGGAGGTGCA GTGAGC	CCAGGCTATAATGTTGTGGGTGCGATCT/CJGCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCCTCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACTAACTAATTTTG TATTTTATAGTAGAGACATTTGATTTTTTAGTAGACAGG
TIGR- A004X20	25	T C GA	---	AAGTTTTCCCTT CTCTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTCCCTCTCTCTGTAGGAT/CJGCTCCTCATGTTACAGTCAACTATAAACATGGCTCATGT TCACCTGGGCTTCGCTCAGAGGATTTGATATTTTGGAAAGTGGTACCTTTGTCTGTGCTTTTCA GACCAACCGCTCTCTTCAATTTCTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATGTCCCAATC ATCATCATGTCTT
TIGR- A004X30	26	T C CCAC	---	TTTGAATCTT AGAGTAGAAC	TTCTTTATGGA AGTGTATAAA CTATTTT	TTTTGAAATCTTAGAGTAGAACCCCACT/CJACTCTAGTAACTTGTATAAAATTAATAGTTTT AAACACTTCCATAAAGAAATAGGGGTGCCAGCTCCTTGATTTCCCTTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102	T G ATGCAAACT	---	TTTGAATCTT AGAGTAGAAC	TTCTTTATGGA AGTGTATAAA CTATTTT	CACGGTATAGCCTTATATAGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCAATTTGGGTATGCAAAACIT/GJTTGCTTTTCAAGAAATTTCTAATATAAGG ACTGTGCTTCTTCATATTCATAGGACATTAACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

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TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGTCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGAGCTTGACACCCCTCTTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTTC/TTCCTCCGATGACCATCTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCCG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAGGCCAGCTTTCAGGCGGGGGGCA GGGTGGGGGAGGTAGGAGACTTC/TGGACCGGACGCCCTGGCTCCAGCTTCATCATCTGTGCTCTT CATCATCTGTGCTCTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC/TCTGTAGATTCTTGGCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG/GCTGTGTAGATTCTTGGCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAAA CTGTGTACAC	TTGTCTATTAT TTAAAGCCCAAC AAAA	CATCAGTAACATATACACAATTGGTCACTCAACTGAACCTTGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACCTGTACACTG/TJTTTGTGGCTTTAAATAATAGACAAATGATTTTG TCTATTACTTAGTGATAGACAAAGTATTACTTTGTTAGACAAAGTATTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACACAGGCCTCTG/AJCTCACAGTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGATAGTACTCTTGGCTGCTTGGCCCTACAAAAGCCACCTTCTAT TTCATACCAATACCTTCTTATTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAAAAAATTTGTTAGGGAAAAAATAATCCAATGGATATATGGGAAGAGAGTG CCAGGCTGGATGGTGTGCTGAGACAGAAATGACCCCTGGGCTCCTTTATTTTGTCTTTTCAACAGGACC CCACAGATAATTTGCGGTATGTCATGAGGACTGGGGATGCTTCTATTG/CJGGAGTCTTCTATT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAGAG/GJCTCAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGTAAAGTATAAAATGTTGTATTTAAGAGAAATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACTACTGCGTATCAGGCACTGACTCGG TGCTTTTAC/GJ/TACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJ/TGCTTAGGGTGTCTCCCAACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGACATTTGTCTGCTTACGGAGCTCCCAAGGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTGTAAAAATTCCTCCCAAGAGCCGCATATGAATCTGCC

X57830	106	G C C T	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTACCTATCTGAAAAAATAATATGAGATTGGA AAAAATTAGACAAGCTAGTGGAAACCAACGATCATATCTGCTATGCCTCATTTTATCTGCAAT GAAAGCGGGGTTCAATGCTACAAATGTGCTTGGAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGAGCTGCTATTTTATATATGACTGCTTTTAAAGAAATTTTGTATTG GATCTG/GATATAAATCTAGATCTCTAATAATTTTAAAGCCAAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTGCCTTATACACAATTCATCTTTCAGCTAATTAAGCCGAAGAAGCCCTGGGAATCAAGTTT GAA
Z48804	44	C T		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTCTCTCATCACAG/C/TTTAGAGCTTCTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAG TCCA
D28513b	133	A G		---	ATGACCAAGCCACCACATTTAGAACCTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGTCAGCACCTTTGGACATGGCTCACAAGCAGTTTGTATTGACTGCATGAATGC/A/ GTTGTCGTGCAAGCATGAACCTTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGCTTC AGCTGTACATA
D29833b	85	A G		---	CCACTCCATCCTGATGCCCCCAAGTTATCCACAGCCTCCTCCCGACCAAGACCTATCCAGCTGGACC TCCATTTTCCCTGTAA/GTTTCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATAATGAA CAACTGCAGCAGGTGCCACCAACCCACAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G		---	CCACTCCATCCTGATGCCCCCA/GGTTATCCACAGCCTCCTCCCGACCAAGACCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATAATGAA CAACTGCAGCAGGTGCCACCAACCCACAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A		---	CTCCCTGCCTCCTCCTCCTGCTGATGCTCCGCTCAACAGCCGAACCTGCTTGCATGGGGGG GAGGGGGGTTTC/GA/JCTTTCCTTCTCTTGGCTCCCTCTTATCTCCACAAACCATTTCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGGCTTTT CTGGA
D37931	64	T C		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/C/ CCGAGGCTCTGCTCCTCAGCTCAATTTCTACTCTTTTCTCTATATAACTCATTTCTATTAATACAT GCACCAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAATAGGCTTCC TTT

D63807	101	CT	---			CAGCAGGACTTCAGTGTCAAGTATCCCTGCCCTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTAGAGGGAGTATTTTCTGTTCAC/C/TAAGAGGAGCTTTTGTTCACAATGGATCAC AATGAGAGGAGTGTCTCTCTCCCTCCCTGCTCGGTGGGAGGGTGACCTGTCCAGATGAC TGGGAACATGCGGTGTGACCTC/C/JACAGCTACCTCTCTCTGAGCTGGTTATGCCAAACAGCCACA CTGTGGGACTCTCTTAAGTTAAATTTAATTTATTTATCTATTTAGTTTATTTATTTATTTTATTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTTCCCTCTGCCCCCTCCACCTCCCTCACAGTGTG TCTGGTG
D90145	21	TC	---			ATTACACTCTCAAAAATTTTGGTGTGTGTTAAGTACTTTCTTATTATGAGCCCC/C/JGAGGA CCAGACATGTTATTATCAAGCCCCCTATATACCATCTAAT
EST14035 1a	59	TC	---			GCATTTTAAAATTCACATTGAATCATTATTACTATTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/TJGTAGATTTTCAAGTGTAGGTGCTCAATACTGAGCACCTTATCT
EST16668 5	71	CT	---			ACAGACTATCGCCCACTTATAATGCTTAACTTTATGATCAATAGTAATAATTTACAC/C/TAAGATA TTCACACTTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCACTGTAGGTTAACAT
EST16904 7	57	CT	---			TTTTAAGTACAGAGGCACTGCTGGAACAGGATGAAACTGATACACCC/C/JGTTACTACTTACTC TTCACCTCTCAAACTGATCCCTAAAGACTTCTACTTAGCATA
EST21863 9	49	AG	---			GGCTGAAGTAGAATCAAGGTTAAGAACATTTTATGCATTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGGAG/JGTGACAGTGAGCAGCAAAAACACAA
EST21885 6	80	GA	---			ATTTAGTGCAATGACAAAGCCCCAA/JGJAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTACACAAAGTATGGGAGT
EST22623 8a	26	AG	---			AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAAATGATTATCCATTATTTACAG/JGJAAATGTGGAAAGATGGCTTTTAAACCC
EST22644 2	98	AG	---			CCTCATTTATTTAAAAGACGGACATAAAAA/T/ATATACAAACAAAAACCCCAAGTCACATTTTCAG GAGGTAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST23587 1	31	TA	---			AAAGATCTGGCATTTACATCATCTTAAATATTTTGTAAATACITTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTACCGTAAATACCC/C/JGAATAACCCATAGTTACAGAAATGG GTCGTGTAACCTCAAT
EST24246 7	106	TC	---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/JGJCATTTAAAAATGTATCAAT GCACCTCTTCAGTACCATGAAATATATAAACCTTCGTC
EST24308 3	45	AG	---			CTTGAACCTCTGGTCTCAAGTGTACGTCGCTCAACCTCCCAAAATGATCGGATTACAGGCATAAG CAGCCG/JATGCCGTGACCCACATTTCTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST24435 6	73	GA	---			TATTGTTGCATTATCAAAATGGTTA/JGJAGTTTCAATTTAAACCTGTAATGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTCCCAATCGTTAGTTAATGCTACAT
EST25089 6	25	TC	---			

EST25476 9	33 GA	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCCTCCTCTAAAAACCAACACA AGAGGTCTCTTGTGCTTTCCTTTCATGGACTGTGGCGGCTGGAGCTTGGACCGTCTGCTGA
EST26183 2	70 TA	---	---	AGATAATGCATTAGAGCTGCCCTCATTTGATCTTGATTAACATTTGTAAAGATTGATCTCTAAATAAG AT[T/A]ACATTTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 TC	---	---	AGAAAAAAGGTGCTACCAAGAACTCATG[T/C]GATAGCGCTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACACACTGTGCTCTAACAAACACGGTGACTCTGA
EST27816 5a	26 TC	---	---	CAACTCAAGGTACAAGACAAATTGCAT[T/C]TAACATTTGTTATAAATAAAAGGAACATCAGATCAAT CAITTAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 AT	---	---	GTTTAAATGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAA ACTTACAATCA/TGGTAGAAGGCCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 AC	---	---	TACTCACCCGACATACATATCTCA[C/G]TAGAATTAGCTATACTGCATACTAACTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACACTTGCTAACTTAAACAAGACAGACTCATTTCTTTTGA G
EST30935 9a	59 CG	---	---	AGCTATGTTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 GA	---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCTCTAAAAACCTGTTGAATAGATAATGGCCAAAT ATTACAGTTTCTCAGCTTCCCTATGAATACTGGCAGCTGTTTATTTCATGTTTATGTGAGTTTCTATGC ATAAAAAATCCAGTAAGA
EST33274 4	27 TC	---	---	TGCTTTGTTCCCTCCAAATCCTAAAA[T/C]GTGTGCTTCAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCAT GGACTAGGTA
EST33352 7b	75 CG	---	---	TACACATTATTCAAGAGACCACCTGACATGCATCTCCTCCGCAAGATACATTCGCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTTACTAAGAGAAATATCTCTGGTGTCATATCTAGGGG
EST33424 1	126 AC	---	---	ATTTTCCCACAGCAGAGAAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTTCAAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[C/A]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 AG	---	---	CCTTTGGGGGAGTTTTAAGCCAGAATGTGACAAAGTCACATTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATATAAGCT GCTC
EST33508 1b	45 CT	---	---	AAAAACATGCTATTGAACAAACTTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACITTTTAGAAGCCAAATAA

EST33508	36 A G ---			AAAAACATGCTATTGAAACAACTTTTATAAAGA[A/G]TAAGTTGACTGAAAGAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAGCCAAATAA
EST33863	77 C T ---			ACAACATAGGACTGGTTATCTTGTTTGAATAATTATGTTGCCACTTCCTATTGTTTAAAAATGA TCATTTAA[C/T]CTTTGAAC[TAGAGCCTGAATCCCCC
EST34739	97 T A ---			GAAGTATCCTCCAGTGGCAGGAAC[TAGAGCCTGAATCCCCC GCTGATAGCTTCTAGGCTGTGGGAACCTC[T/A]GGTGCCTTACAACCTCACTGCAGAAATTTCT TGTTGTGCCTCATAAACA
EST34792	104 A G ---			ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCAGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GATTTCAGGAATTTCTTAGTCTATTACA AAGATTTGTGCTGTG
EST34835	93 T G ---			GGAAATGTTCCCTTTGCAACAAGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGTT[G/G]GCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835	82 G A ---			GGAAATGTTCCCTTTGCAACAAGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGCTTTCTGTTGGCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230	93 G T ---			CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGACATAAAAGAGTTCT[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337	33 C T ---			TCCTTTCAAATTTTGTAGGCATTTAATG[C/T]TATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACITTTTCAATTTTCATCT
EST35708	32 C T ---			CTGCCCCAAATTAACITTTAGGCAATGGAAC[C/T]AGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGACGCGTGTGCTCCCTCTCTGAGGTTGGCACCTTTCTGTTGTG ATGTGCAAGTGTGGCT
EST35747	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT G
EST35751	89 C A ---			TGGTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTCAATGGAGA AGTTCCTCCCATGAACCAAGA[C/A]CTTGCTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAGGCCCTGTGA
EST36301	93 C T ---			CACCTGTTCAITGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTGAGCCTACAGC AGTCAGGAGGCAAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAAACA
EST36519	33 G T ---			GCCATCAGCCACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACITTTGACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTCTCTGT CACAGGGTCTTAGTCGT

EST36620 6	50 G A ---	---	GAC TTT ATT AGA TAA GGG GTT CGG CTAC CC TCA AAG CTCTC AGG ACT GG [G/A] GCTAG GGT TTA AGG AAG GC TTA TTT AAATAT GGG AAAT AAAA TACA AAG GGG CCA CAC CC GATG CAAA AGACT TT
EST36690 0a	89 C G ---	---	CCT GTG ATG CAT GGG TGC CTG AGC AGT CGT ACT TACT ATG CGT CAG ACAG CTCA CGT ATG TCAG GA AAG GA AGT CTG GGG ATTCCTA [C/G] AGG GGC ATATC ACAC ATATTCTA AGTCA CTGTG TGA CTGGG CTTGAG CAAGTCATTTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCCTCTCCCTCTAATAATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCAC TTTAGCTACCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTAIGTAAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACA ACTGACATTTTGATGAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTCACTCTCTTGCCCGAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGTACGGGCCCGTGGGATGTTAAAAATGGGATTTTAAATTAAAGATTGTGAACATG CAAA CCCAGCAA TTTCTCAGCTTATATTTTGAAGTCT[T/G]CAGGAGAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGGAA GCTCTCTGGATAATGTCACTCTAGGA[A/G]TAGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCT CTTGGCTTGCTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAAC TAAAGATATCCTCTGCCTCAGCCTCCAGGTAGT TGGA ACTATAGTAGGAGTATCTT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCCTCTCAAACTT[C/T]AAGGGTGAAGAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTACATAGCCACACATTTTCAAGGCAC TCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGT[C/G]GAGCGCTGGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCAGAGTGTGTGCTCCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGT[C/G]GAGCGCTGGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCAGAGTGTGTGCTCCTGCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63	T G	---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCGTGAAAAAC[T/G JAACATGCCTCAAAAAAGAGGGGAAAAAACCTTTAACAGAAAACTGTGCTGACATGATTAGCTT
EST37452 4	46	G A	---			AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAAAACACCCTTAAATCAATGACGTAGAA
EST37613 6	34	A G	---			CTAGGCATGGGGCTTTACAGTCATTTATTACC[G/G]GTCATGAATTCATTTAAAAACCCACAGCGAT ATAGCAATGAGCAAAACAGAGCCCTCCCAAAATCACCCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56	T G	---			TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTA[T/G]TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCTCGCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57	C T	---			TCTACGAGTCCACAAAGTATCTGTATATGCTTTAAGTGGCATTTCATGTCACCTTA[C/T]CGCATGG AAGAAGCTCTCCTTTTAAATCCCTAACTCTCTCTCTGGGAAGACAGAACGTCACAA
EST38420 6a	100	T C	---			TAAATCAAGGCTCTTTTCATTACCAAAACAAAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCTCCTGACTGAC[T/G]TCCCTGCAGTGCCCATGGTCCCGTGCCT TATTCTCTCCTCTCTCA
EST38950 5	25	T C	---			TTTATTGCAAAAGTAAGCAGCGGT[C/T]GGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90	T C	---			TTTTTTGTAAGTCTGTAGCCAGTCATTAATCTGAAGGTTTAAATATATCATTTTATTGGGATGAGATCA TAGCTTTTACACAAATGCTATG[T/C]AAACAAGTTACTGAATATTTTCACTCGTGGAGTTG
EST39331 1	70	G C	---			TCCTTCTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TG[G/C]GTGTTTAGGGAGAGCTGGCACCTGGCCTCTAAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C A	---			GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCCTAGAACCTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37	T C	---			TTCTAATAGCATGCCCTGTGACAGGGAACTAAGCTCT[C/T]CAAAATAACTGAAACTAAATCTGTA AGATAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTG AATACTGTGGGACTCA
EST40549 1	42	A G	---			TGTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCAC[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCCACCTTCTCATTGAACTAGCTCCCTGCAAGCACCTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81	A C	---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCATTCTTACCTAAAGTCTGTCTATCTG AGCTGGTGGAA[A/G]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTTCCAGGAAG
EST40584 3	68	A G	---			TTGATGGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTAAAGCT

EST51340	51 G A	GATCAAACTGTATTGCCAGGCGAGCTCCTGAAGAACTGTGAACATATGAAC[G]ATJCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTITTCCTTTGGTCTCCAGTGGGAAGGGAAGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63 T C	CTGAACCTCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTCTCAGCTTCATGTGAAACCTAC[T/C] CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTTATCCATTACCTCAAAGCAGTCATTCTCT TAGTAAAGTTTCCAACAATAGAAATTAATGACACTTTGGTAGCACCTAATATGGAGATTATCCTTTTC ATTGAGCCTTTATCCT
L18877	69 T C	TGAGTCTGAGCAGGAGTTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGGCCAGTGCACCTTCCAAAGGOC C[T/C]ATCCATTAGTTTCCACTGCCCTGCTGTGACATGAGGCCCATTTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C	GCTATTTACATATCCCAAGCCCTTTAGGGCTACAG[T/C]CTCTGCTGGACCCCTGTAGGGTGCCA TTTGGAGTTTACAGCCTAGAAGAAAGGCTTTGGCCCTGGTGTGGCATAGCCCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C	GGGTCCAGAAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACCCAGCGTCCCCAC CC[G/C]GCTCGTGTGTAGTATAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G	ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTAGTTCTTTTGTATTTTGTATATTTGJCGCCTGA AGATATCCCGCAAGCAGGCTGGAGGTGCCGTGGCTGTGTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173 G A	CAAAGTTGCTCTCTGCCCATGAGCACACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAAACAGC CCTGTCTCAAACCTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCCTCACACCCACAAATCTGAAC[G]ATJGCTCTCTCCCTTGTCTTACAAATGTCT AAGT

L48728b	111 T C ---	---	AAGTGAACAGAAAGATGGATTGTTCCCTATAAAAGCACATAGTATGTTTACTGGIATCGT AAGAAGCTGGAAGAGAGCTCAAGTTTTTGGTTTACTTTTCAGAA/T/CJGAAGAAGTATTCAGAAAG CAGAAAATATCAATGAGCGATTTTAGCCCAATGCTCCAAAAGTCTCATCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	GCGCACAGTCCAAAATACAAATGGACAGAAAGATCTATATTGTACAGAACT/G/AJTTTATTTACCC CCATCAAGTATAAGGTTACTGATTGTTGTCCTTTTATAAACATTGGTATATTTCCATTTCATGCCAA AGCAAAAGAGTAAAGCTAA
M19169	113 T C ---	---	TAGGATCTGTGCCAGGCCATTGACACAGCCACCCACTCCACCCCTGTAGTGTCCACCCCC TGGACTGGTGGCCCCACCCCTGGGGAGGCCCTCCCATGTGCTGT/CJGCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCCTCCTTCTCGCTTCTAATA GC
M21539	114 T G ---	---	TCACCTGTTCCACAGCTCCACCTGCATCTTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATATCCCGACAGCAAA/T/GJTTTTCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCCCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---	---	CCTAGCATATTTCGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTCCTGACTTC CTGATTTTCTTTCTCTCA/JGJGTACCTACTAAG/JGJGATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	CCTAGCATATTTCGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTCCTGACTTC CTGATTTTCTTTCTCTCA/JGJGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	CCTAGCATATTTCGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCC TCTTCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTCCTGACT TTCCGTGATTTTCTTTCTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	TAGGCAGCTGTACGGAGGCCAGTCACAGTCCAGCAATCCACAACCACCTTGAC/G/JAATGCT TGCCAAAGCTGTTTAAAGCCAAAGAACACCCCTTCTTTGTTCCAAATTAACCTTGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---	---	ACTTACTTACCCTCACCTGTACGGTGCAGGGGA/JAAGAACCTGCACCCAGAGAGGCTGGG ATGGCCTGCTCTCTGCTTTGGGAGAAAACGCTGTGCTGGGAGGGCCCTTGTGTGCAAGGTTG CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTCCCCCAAGGAGCTTGACTTGCAATTTCTACC T

U06641d	166	C T ---	---	CTCCTCCTTTATTCAGCATGGAGGTTTAAATGGAGGATCCTTTTCTGTGACAAAACATCTTC ACAACCTACCTTGTAAAGACAAATTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAAAT TATTTCCAGGCTATTAAATACGTACTTTAG[C/][T]GGAATATTCTATGTCAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39	T C ---	---	GAGGCCTTATGAGGTCCTCTACTCAGGAACACCCCAAT[C/G]ACATTCGATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTAAAGTTCAAGACAGATGGGCATATGTGCAG TGGGGCTCTCTGAGTCTCTGAGTCTGGCCCAAGAGCAAGGAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C ---	---	GAGCAAGAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C/J]ACATCTGCCGCCCTTCCAGCCCTTCCCGAGCCCTCCTCTGTGTTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	C G ---	---	GTGACATGAGGCCCATCTTC[G/G]CTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTTCTCTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGTCAGTTAATGAACCTTACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C ---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGACAAAGTTGTTAAC CTCTTTGTTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAAAGAGAT[C/J]TACCCTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187	T C ---	---	TTCTGTCCACTTTACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C/J]TGGTCTCATAC CTCATATGCAGGATTCATCA
U17077	122	T C ---	---	TCCAATATTGGTCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCTTGCAGACTGAGCGATGACACCACAC[C/J]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTGGGAAAACAACTGCTCTTGG AATTA
U18543	58	T C ---	---	GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCAGCTGGGTAGTTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTATTTGTTATGTCCCTCCCGCTCCCGCTCCCACTAAATTTAGAGCTTTAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/C/AAGATATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTTGTGGACTGA
U25975a	143	C G ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG AAGACAAC/C/GAAGAGAAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTTGTGGACTGA
U25997	61	A G ---	---	CAGGGAGAGGTTATTCAACACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA/C/GJTT TTGAGTGTACTGTGCTGGTTTGATTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAGAAAAAT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCACCAACAAAA TCC
U28413	29	C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATAATTTTCCTCATGTTTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTTCCCTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCAATTGCTACAGTACAAAGTAAACAAAGTCGTTGTACCTCAGTT G
U30884c	89	A G ---	---	TAGGGGTAGCATTTAAGATTTCAGGAGTCATTAGCAGTGTGATGATTTTGGGACCTGCCGTATAATCTGT CTTCTATTCCACAGTTAGCCA/C/GJTTGTTCTTGATGAATCTATATGATGATAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U30884a	34	A G ---	---	TAGGGGTAGCATTTAAGATTTCAGGAGTCATTAGC/C/GJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTCCACAGTTAGCCAATTTGTTCTTGATGAATCTATATGATGATAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAGT GCTGTCA
U31216b	78	A G ---	---	GGGACAGCATATGTGGCACCGCCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCCTGCAACCAACA GCCGTCAATCA/C/GJCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACAACTAGAGGAGGAGGAGGATGCCAGCGGATTTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A ---	---	GGGACAGCATATGTGGCACCGCCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCCTGCAACCAACA GCC/GA/JTCATCAAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACAACTAGAGGAGGAGGAGGATGCCAGCGGATTTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ---			AGTTGCCAGCTCCCATGTACACGAGCTGGAATCTGAAGGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC(G)ACACAAATCTGGTGCCTCTCTCTTGTCTTACAAATGTCTAGTCCCACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---			AGTTGCCAGCTCCCATGTACACGAGCTGGAATCTGAAGGGTGAGTCTTCATCTTAGGGCATCGCTC [C/TTCTCAGCCACAAATCTGGTGCCTCTCTCTTGTCTTACAAATGTCTAGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---			ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCTCTC AGACCGCAGG(C/TTCCCAAGCTCAGGTTGCTGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAAAGCAAGGCTTGTCTTCTATCTGGGGACGCTGCTCGAGAGAGCCGAGAGGCCGCGAAGC ATGCCAGGTGTCC
U37690	54 A G ---			GACCACGCTGAACCCACCCACCCGCTGTGCTGACCATGGCCCTGAGCGTCTA/GJCCCGGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGGTAATGCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---			TGAACCGTTTCAACATGGAATGATCTGTATTGACTAA(T/C)ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCAITTTCTCTATAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---			TCAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTAA(A/T)ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCTCTCTGTTTTTTCATGTCCTCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ---			AGGAAGATCCACCGACCTTCTGACCTAATCCTTTAGATTAGGTCACATTACATTAAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGGAAGGAGACACATTCACAAAGAAAGTTGGGAAATTTGCG AAATCTGTTGTGCA(C/T)GCTCAATGAAAACGCCCTTCGGCTTTTATTTTTTTTGGAAGTGTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A/C ---			AGGAAGATCCACCGACCTTCTGACCTAATCCTTTAGATTAGGTCACATTACATTAAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGGAAGGAGACACATTCACAAAGAA(A/C)GTTGGGAAATTT GCGAAATCTGTTGTGACGCTCAATGAAAACGCCCTTCGGCTTTTATTTTTTTTGGAAGTGTG CGAGTGGCTTAGGCTAGCCT

X54741	24	A	G	---	---	CAGGCCACCTGTCTTCTCTCCAC/GJTGACAGCTTCTGAGTACACCCCTGTGTCCAGGCAGCTCCT GCACAAATGGAATCCGAGGGCTCCAGGACTGGGGCTTGCAGGCTTGTCAATAGCAAGGCCAG GGCAGACTGGAGACGATCTTGTGGCAGGGCTGGCCTTGTCCCAGCCCCACCTGGCCCCCTTCTCC
						AGCAAGCAGTGC
X54869	99	A	G	---	---	AAGCATTGGCTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTATTTATTTGCTCTAGATACAAAAATCTAAATCAATTTATTGAAATAG GATGCACAAATTAATAAGTACAGACATCTAGCATTTGTGCGGCTCATTTTGTCAACATGGTA
X6924	147	G	A	---	---	GGCTGTCTGCACACCTCCAGAACGCGAGTGTGGGCGGCTTCTGCTGGGACCCCGGGAACCTCTC CTGCCGAAGCCGAGCGGAGTGGGCCCCAACTTCGCCCTGCCCACTTGACTTCACCAATCCCT TCCTGGAGACTG/AJAACTGGTGCTCAGGAGCGAAGGACTGTGAACCTGTGGCTGAAGAGCCAGA
X78932	62	T	G	---	---	GAAATGTGAAGAATGTGACAAAGCCTTAAAGGGTGTACACCTTGATTGTATATAAGATAAT/GJT CATACTGGAGAAATCCAGAACTGACAAATGTGACAAACATTTAAATTAATCTCATACCTTA TTGCACAGGAAGCATTATACCTGAGAAAAATTTGTATAAGAAATGAAAAAGTCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25	T	C	---	---	CTCAACCCATAACCTCAACCACATCT/GJATCTCTCCACCCACATCCACCCACATCCACCTCCATCC CGAACCCATCTCATCCCCAACTACAGCCCCAAAGCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80197b	99	G	C	---	---	ACCCAACTCAAGTCCAGGCCCCAGGCATCTTCTGCCCCCTGCTTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTGAGTACTTCTCTG/CJACATTTGAAAGACCCCTCCCACTCTCTGGCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28	A	G	---	---	ACCCAACTCAAGTCCAGGCCCCAGG/GJCTTCTCTGCCCCCTGCTTGGCCCATCCAGTCC AGGGCCTGGAGCAAGTGTGAGTACTTCTCTGCACTTTGAAAGACCCCTCCCACTCTCTGGCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X85106	150	G	A	---	---	GGCACCGAGTGAACCAAGTCCAGAGGGAGGGCGGCCCTCGCCGTGTCCGTGTTTCTTTT CAGCCCCGGAGAGTCTGACCTGGGGCTTCTCCAAAGCTCACTGCGCCACGCTCCCCGCCCTCT CTTTCTCCAAAGC/GJAAACCAATGCGCCCCCTTCACTCGCGCTGCGAGGCCGGGGCTT CTTTCAGAGC
X87160	128	T	G	---	---	ACCACGACCATGGTCTAAGGACATGGATCGGGTGGCCCCAGACGTGTGCACAGGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA

[illegible]

1282	130 C T	---	---	GTGGATCACCACACAGTCTAATTTTCAGATGTTTCAATACCCCTAAAGAAATCTTTGACCCATTAGCAATTTCTCTATTCCTGCCCTACCCCGGCCCTACTCTTTATCGCTATAGATTGGCCTGACTTGACATATCATACACATGGAGCCCATACATATGTGCCCCCTCATGATTGGCTCTTTCACTGAGAATAATGTTTTCAAGGT
6810	68 C T	---	---	AGTATCACACATACCTAATATATTAGATATACACATAATAAATCACCTCCCTACCTTGAAACCTTTA/C/TAAGAGCATTTTAAATTTACAACAAAGCTCAACGAACCTACAATAAGTCTAGTAGCTGTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTAAAAATGCTATGAACAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACCACTAAGAAATATTTTTAAAGGC
6817	118 A C	---	---	CCAAATACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCATCACTCACTCAACAATGTAGCTGCAGGGTAAC/C/CTGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGATCATCAAGAGATTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGGGCCGTGTCAGATCGGCTTTTGGTTGGTCTTAG
6819b	212 C	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAAAGACTTAAATGGAAACATTTAGTACCATCATGTCA CCGTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166 G T	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAAAGACTTAAATGGAAACATTTAGTACCATCATGTCA CCGTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGC TTAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39 A G	---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTGTTTATCTATGCGACCAATTTGGGACA CAGATTATATATGTCAGACACCAAGCAATGTCTTTAAGATATGCGAAGCACAATCTGTCATGGT TTAACAAAAGAAATGAACGCTAGG
6972b	149 G T	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTCTGGACTCTTTTGGTTGGTAAACTATTGATTATG CACAAATTCAGAG/GTCCCTGTTATTGGTCTATTCAGAGATTCAACTCTTCTGCTGGTTAGTCTTGGGA GAGTGTATGTGCGAGGAAT
6972a	122 A G	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTCTGGACTCTTTTGGTTGGTAA/GTCTATTGATTA TTGCCACAAATTCAGAGCCGTGTTATTGGTCTATTCAGAGATTCAACTCTTCTGCTGGTTAGTCTTGGGA GAGTGTATGTGCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAAGTTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACACCCAAAGCCAJAG/AGGAAC TCAATGAAATAAGCCGTAACCCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACAC/AG/CCAAAGCCAAAGGAAC TCAATGAAATAAGCCGTAACCCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTJAG/JGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGTAACCCAGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCTT TTAATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAAATGAATGGGTGAGTCTATCTCTCAAGGTCCCAATA/ATJCCCTTGAGGTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAAATGAATGGGTGAGTCTTJAG/CTCTCAAGGTCCCAATAACCTTGAGGTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTJATGATGAATGGGTGAGTCTATCTCTCAAGGTCCCAATAACCTTGAGGTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAAATGGGTCCCAATAAAATGGAATTTTAGGGCAACAAAGCTAAAGGCCJAG/CAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGSAATC TGGGTTTCCCTCTGAATTCACACAGAGCATGCACATACACACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCCCTACGGAGAACTGGGAAATCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTAA/CTJGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCCCTACGGAGAACTGGGAAATCTGGATATTTGGCTTATCATT TG/AG/CGCAAAATCCACTTTGCTGTAACTGTAACGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAGGAAAAATTACTG
8498	84 C T ---	---	AAGGCTTCAGGGTTGGTTTAAATCAGGCTGCACACTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/CTJAAATCTTCATTAAATCGAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCTATGTTGCT TTATACATCTCTCTCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A ---	CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAGTAG CTTCTTTATTTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCATTACATT TAGCATTAATCAGAAACGA
WI-18618	51	A C ---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAA[C/A]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCTTCGATGCCAAAGTATAATTGTAACCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---	TAAGCTGTTCAAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75	G A ---	GACTTGGTGATTAAATTGCTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94	A G ---	AAATAAGTTTTATTGGCACACAGCCCAAGCCCACTGGATGACACATTTGTCCACGGCTCATCTTGCAG TACAATAGCAGGGTTCACTAATGTAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATAAT
WI-18582b	69	T A ---	GTCTATTTCAAATTTAGCTAGACCCATTTCACTCTGTTTAATGGCTACATTTGTTTTCATTGTGAGAC T[A/GTGCCATAATTTATTAATCAGTGCATATTGAAAGACATTTGGATCGTTTCCAG
WI-18723f	94	G A ---	AACTTATTGTATCTGACGATCAGCGATTAGTTCTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---	AACTTATTGTATCTGACGATCAGCGATTAGTTCTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/AACAGGTACATAGGTAAACCAAATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G ---	AACTTATTGTATCTGACGATCAGCGATTAGTTCTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---	TTTATTACAATATTAGGTGGCACAAATAAACAAGCTTCTGA[G/A]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACCTCGAAATA
WI-18715	76	G A ---	TTATTCAAAAAAGTGATATTGCAGAGGTTCTGGGGCTGTACATGGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGAGCCTCCAGGTGAAGGGTATTTTTTAATAAAAAATAA TGGAGCTACAACACACCC
WI-18535	107	G A ---	GTAAATAAAGTTTTATTGGCACAGCACGCTCGTTTCAATTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGTCOCOCGTG
D17525	107	C T ---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTAGTTCAGTTCTGGCAGGTGAC TTTATCTCTTCGAACCTCAGTTTCTTCATAAGATGGAA[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTGCTACCAAGGCAGACGAAG

DWU-133c	313	A G	---	---	TAATTGGCCACTGCCCTTATTATTACAAACAGAAATGTCATGACTTTTATGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGATAATTTGTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTACCCCTTTAAAGATATGATTAGACT
DWU-133b	236	T C	---	---	TAATTGGCCACTGCCCTTATTATTACAAACAGAAATGTCATGACTTTTATGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGATAATTTGTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTACCCCTTTAAAGATATGATTAGACT
DWU-133a	199	C T	---	---	TAATTGGCCACTGCCCTTATTATTACAAACAGAAATGTCATGACTTTTATGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGATAATTTGTTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTC ITCCAATTCAGTAAATGGTATCACTCGTTACCCCTTTAAAGATATGATTAGACT
DWU-36	102	C T	---	---	ATGAGATCCTTTAATCCTTCATGAACGTTTGTGGTGGCACCTCCTACGTCAACATGAAGTG TGTTCCCTTCAGTGCACTGGGAAGATTCTACCCCTGACCAACAGTTCCTCAGCTCCATTTCGCC CCTCATTTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T	---	---	GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTAGTTTAAACTGCAGTCCCAACAGTTCATTCATATATAAAGCATTATTTTAA CTCTTTGAGGTGAATATAATTTATATTAACAATGCTGTAAGAGCTTCTTAATACTAAGTATTTTCA GGTCTTCAACCAAGTATCAAAAGTAATAACACAAATGAAGTGCATTATTCAA
DWU-447b	172	---	---	---	ATTTAGTGCTTTGCGTTAAAAATCATTGCAAAAGTATTCGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATAGTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTGTAG GCCTTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G	---	---	ATTTAGTGCTTTGCGTTAAAAATCATTGCAAAAGTATTCGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAAAGTACTGTAAATTAATAGTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTG TTAGGCTTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G	---	---	GTAATTCAGTTTTCAGTTCCTCTTTGTGCTGCTTCTCAATTAAGCGTTTAAAGTGAGCTGAT AATCAACTGTCCATCAGGTGAGGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAAATTCATACCATACAAAAATTA A/TJGCGAGTATTTATGTTTAAAGCACAGGTGTACCGAAAACTGTGAAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	AAAAATCCAGGCATTTCGAATCTGTTTTCATGATTATAGAGGGTTTACACAAAGTGCCACTTATTA AGAGCTTCCACAGTGAAGATGGAGAGGTGAACCTTGTGTTGAATATCCAGATGTTTGGTC A/G TGCGTATGGCAGTGAGCAGGTATGTTGCTTTTGTCTGCACTGAAAAATTAATTTGCTATCAAGAGC AAACTATGAACGGTTTTATTCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTCTTCTATACTGTTTGT ATATACAGTTTGTAAACCATATGATTGA A/C AAGAAGAAAACTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATTCCTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATTCAGTCTCTGATTTCG
DWU-59	94 C T ---	---	CATTTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAACATGCTGAGAAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTACATTGGC C/T GAGCCGTGTTCAAGTCCACAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTTAACTTCCAAAGGTGTTTACTTCTGTATAGCCGGTGAATTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	CTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	CACACTGGCATCTAGGCCCTTCGCTGCATTGCAGAAAGGAGAGCCAGGTCCCTCCCTGGAGAA C/T G CTGCGTTCCCGAGCCCAACACCGGCTTGCACACACAGGCTGTTGAGGCAGGAGGTGGGTAAGACGT AGCTGTAGACCCAAAGCAACCAACCGCCTGGGACCCCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCAATCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA A/G GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTTCTATAA T/A CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT C AAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCTATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	TGTAAGGTGACTTCTATAGCTTCCCTAAACTGCAAACTTTTCAATTTACTGAGATTTATTCAGGCCAAT GTG C/T TTGGGTCTGAGATTGATTATCAGCTGGGTAAGTTAACCTGTTCTCTGTTTCA

WI-18063	105	G A	---			AGGCTTTAACTGATAACAATTTGCCCTTAATACACATACAAAAACTCGACATTCCTTCCTTC
					---	CCATGTTTCTGATTTTGATGTAACCTTAAATTTGTGATCCCTTAAACAATATACGTAGCTGCA
WI-18078	86	A T	---			AGTTGAAAGATCAGAGAGGTTATGGTGGTAGTAGCTGAACCTCAGATTCAACCTGGTCCAGTGTG
					---	TGTTTTTTCAGCATCAGATGTCCACTAGCCAAGTTGATCTCGCAGTATCTACATGTGGT
WI-18091	90	T C	---			CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTCATCCCTTTTGTAAATCCATCAGACACTGTGGT
					---	TTTCATCTCTAGAAGTTGACTTTCGGGCTTTTATACCTCCATATCTCAACTTGTAAAGC
WI-18119	38	T C	---			GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGATTCJTTGTAAATGGATTGGAGTACTTAC
					---	CACATTTTCATCTGCTCTGAAATAGTTCACCTAACCAACTACTGACAAACAGTTTAAITTTGGTCTT
WI-18142	66	T G	---			TTCAAGATAATTACAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAAATAATCTATATAC
					---	T/GJCCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAAGAGGAAAA
WI-18178	68	T C	---			GCATAGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAGTCCATCGCTGGAGGTTAGTCTGGGGG
					---	GT/CJCGGCGGGATGGACACACAGACACACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	G T	---			TCAATCTGAAAACCTTGTGTAGCCAGCATGGGGTGTGGGGAGGTGATTATGGCTGGGGAAGATG
					---	GGCACTCACCGACAGCAGCATCTAGCACCACAGTACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A	---			ACAGATGTCAGTTGTTGAAATGGCCATTAAAGTATGGGGCTTTCTTGTAAAAAGTCATCCAAA
					---	AGGCTTGGCAAGAGTTTGCTATACAACGGAGGACAGAGAAACATGA/GA/JCTGGGGAGTAGGCTCT
					---	GACAGAAAGTGGGGTGTG
WI-18261	26	G A	---			GATTTGAAGGGATTGCTTTTAACTTAACTGAAAGCGGTGATAGAGGAACIGTTTAAGATAAACAA
					---	CTTATAAATACTCCCAATTGTAGAAGTGAAGATTG
WI-18268	88	C T	---			TAGGAGGAAAAAGGAGGTGGGCTGCCCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC
					---	TTCCTTACTTCCCCCATAGATCTTCCCTGACAATGTGCTGCAGAAAGCCTCCAACTGGAAC
WI-18299f	107	C A	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTGGCCAAATTTTT
					---	ATCTATTTGGGTCTGAGAAATCCACAAATTTTGA/GA/JGAATCTTTTGGCCAAATTTGACATATCTG
WI-18299e	101	A G	---			CAG
WI-18299d	77	G A	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTGGCCAAATTTTT
					---	ATCTATTTG/GA/JGCTGAGAAATCCACAAATTTTGAAGAATCTTTTGGCCAAATTTGACATATCTG
WI-18299c	67	T G	---			CAG
					---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTGGCCAAATTTTT
					---	T/GJATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAATCTTTTGGCCAAATTTGACATATCTG

WI-18299b	52	G A	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[G/A]TTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATATTGACATATTCCTG CAG
WI-18299a	48	C T	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/]TTGGTTTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATATTGACATATTCCTG CAG
WI-18307	76	G A	---			TCAACTTGTACCAAGTTAGCAGCAAGAGGATACCTTCCCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTTGGTCAC
WI-18324	72	C T	---			TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGGTACTGATT TAT[C/]JTAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C	---			ATGAAAGTCACCTTCAATCATAGGGTCAAGAGAAAGAAATGTTTTCAGA[T/C]TAAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACACACAAGTCA
WI-18395	77	G C	---			TCCTGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTCCTGGAAAAATTTGAAGAAATAAAATTG ATTATTCAAAG[G/C]JTGTCATTGGTTTATACATATCTCTCTCTCTTAATGCAAGCTATG
WI-18398	62	G T	---			TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21	C A	---			CTCGTTGGTATTCCTCATCC[C/A]TTCCCTTTTCGCTCTTTTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAAAGTC AATGAAAA
WI-18409a	20	C A	---			AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTTTCCCTTTTAAATCTTTTCAAAAT TCAAGGATCATCAAGGAGCAGGTGCAGAAAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
WI-18442	62	C T	---			AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGACAGAGAGGAACAAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGGAAACACAAAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38	G A	---			TTGATGTTAATACTGTCTGAGATCGGCTAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGG TATAATCTCGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTTCCAAACCA
WI-18489	102	A C	---			ATATAAGCTGGAGACTGTGGAGGTGAGAGGCGAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93	A	---			CTGGTGGGAGGAAACAAATTTGGTATATTCATACAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAAACTGTAATCACACACATGGACAAATCTCAAATCATATTGCTGATGGAAAGAAACCATTCATCA TAAGAATACACAGTACAT

EST5	93 A	---			CTGGTGGGAGGAAACAAATTGGTGATATTCATACAAATGGAAACTCTTCAGAAATAAGAGGAA CAAAACCACTGAATCACACAAACATGGACAAATCTCAAATCATATTGCTGATGGAAAGAAACCAATCA TAAGAATACACAGTACAT
EST6	48 C	---			TTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAAACAAAGCTTTCTTCCCTTTTCAACAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A	---			GGACAGGACCTCTATTCGCCCTGGTGCAGCAGCGGTGATGGACTGAGGCCCGCCAGGGATCTGGGCC CTCTCTCAGGGGGCTCCAGGACCCAGAGCTGTTCTGCTTTGAGTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGCATGGAGATTTGGACACTGTGTGCTTTGGTGGGGT
WI- 18740c	104 G	T	---		TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCATTTACCATCATGTATC/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C	G	---		TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCATTTACCATCATGTATC/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C	T	---		CCAAAGTCTCTGTTGGTCTATAAAGAGTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCAATTTACAGAGGTAGCACAA/CJTTGATTCCAACAAACCCCTTCCCC TTTTTAAATGATTCTGTTCTAATGCCATAGATCAAAAGGCTCAGAAACCATTTGTGTTTCCCTCTT TGAAGCAATGACAAGCACITTTACITTCACGGTGGTTTGTGTTTCTTAT
WI-18746	114 G	A	---		GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTAAGTCTGACCGTTTATATTACTTTTGTAAATATCTT/GJATCCACATTTCTAGTTCAAGCT TTGGATGGTTACOG
WI-19112j	212 G	A	---		CCGTGTTACACACACAAATGGCAAGCATAGTCGCCTGGTTACGGCCCGAGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGTCTATCTCATGACAACCAAGAAACCGACGACAAA TCTTTTGGAGATTTTCTAGTGGCTTAGAAACATGGCTTTTAAAGAACACGGTGATATCTTTGAG GGTGACAAGGC/GJATCTCTCAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 A	C	---		TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCCTATAGAAGGCTATTTCTAGATCATGT CTCAATGGAAACACTCTTCTTTAGCCCTTACTTGAATCTTGCTATAATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATATTTTC/AJATGATTAGCCGTGTAAC
WI-19057i	175 G	A	---		CCCATTTATTATAGCCAGTGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTTCAACTCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGACGTCCAGGCCCGCAGCCACTG TCTTCATGCAAGAACACAGTGGCCAGATCCCCACAGCT/GJATCTCTTTCATCTTGGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTCCAACTCAGAGGATGTGGGAATCCCAAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGTCAAAAGTCTTATCCAGATGGTCCAGGTACAG TGGGCTTCCTGGGCTGGAAAGCTGGTCTCCCA[C/T]TTCATTCTGCTCAAAGCTCTTTGAAGGAGC TGGTTTGACTTCAACTTGTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAAATCTTGAAGGACAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A G	---			TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGCTTTTAACTGAGTTTAAAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTGTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165	A G	---			GTCCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA[A/G]AAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGCAGGTAATA[A/G]TATAACATTAGAAAA GCAAAAATCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCACACTGGAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCCTTGGAACCTGCAACGACTGTCCATGCTCTGTGGGGACTTACACATTCAAGTTTGACAG T[C]TGAAAAACCAACTGGAGCTGCTTTCCAAAGAATGTTCTGTGCTTCAAAATAGGAATCCATG TTATTTCTTCTTGCCTTAAAGCTTTATATCTTTTCAAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACCTCCCATCCCGTAAGACCTCCTTCCCTTCCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCCTATTGCATCCCAAAACACGCCCTCTTGACCAGGCTGCCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTGCCTTTTAAAGTAAAAATGGTCAGAAAGAGGCACC[G/A]GGAAAGCCG TCTGGCGCCTGCCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAGGAGCGAGCAT GTCGTGGACACACACAGACTATTTTAGATTTTCTTTTGGCTTTTGAACC

WI-20146	31 T C ---			---	TGAGTCTTCTGTGAATTCATTGAGCAGTTAGCTGCATTTGAGATAAAGTCAAATGCCAAACACTAGCTCTGTATTAATCCCATCACTACTGGTAAAGCCTCAITTTGAATGTGGAATTCATACAGGC
WI-18922	74 G A ---			---	TAGGAATTGGTTTACGCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGC[G/AT]CTGGCTCTAATTCACAGTGTCTTTCTCTCCTCACTGTATCCAGGTTCCCTCCACAGAGAGCCACCACTCTC
WI-18763b	53 A G ---			---	TTCTGTGTGTGGGTCAACCGTACAAATGGTGTGGGAATGACGATGATGTGA[G/AT]TATTAGAATGTACCATATTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38 A G ---			---	TGTGTTTGGCAA
WI-18771b	75 G A ---			---	TTCTGTGTGTGGGTCAACCGTACAAATGGTGTGGGA[G/AT]GACGATGATGTGAATTTAGAATGTACCATATTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771a	57 A G ---			---	TGTGTTTGGCAA
WI-18820	70 T C ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAGATGTTGGGAAACAGAA[G/AA]ATAAACTGAGTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGGA
WI-18742b	51 C T ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAGATGTTGGGAACAGAAATAAACTGAGTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGGA
WI-18882	94 C T ---			---	GGGAAAAATTTGAGACGCAATACCAATAGTTAGGATTTGGTCTGGTGTGATGAAATTCGTGAGGCCT[G/AT]GATTTAAATCTTTCAATGATTGTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
WI-19970b	167 G A ---			---	ACAAAGTCCTGTAGCCCCCTCACCTTTCTGTTTTCACITTTGCCAATGTAG[C/AT]TCGGGTTTGTTTTCTTGATTTAAACGGTTGTGGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA
WI-19970a	126 T C ---			---	GTTTACC
				---	GTGTGTCAAAAATGGGGTCTGCTCTGCTACCTTGACCTTCCCTTCCCTGCTCTCTCTCTCATCA
				---	TCATTTCCCAACAACATCCTCTGCCA[C/AT]ACACAACAAACGTAAGTTTCATTTGGGCAAAAAATTGAC
				---	CC
				---	TATAAGCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCTTCCCTGCCAGTTCCCTACTGCGGGGAOC
				---	AGCAAAAGCCCTTCTCACTGGGTTGGTCAAAG[G/AT]AGTCACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA
				---	TATAAGCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCTTCCCTGCCAGTTCCCTCACTGCGGGG
				---	ACAGCAAAAGGCTTCTCACTGGGTTGGTCAAAGGTAGTAGCTTGGCTTGGCTGCATCCACAGAGGATGTTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCCAGAGACTGCCTCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGGCTCGGAGATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAAA[7] GACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCCAGAGACTGCCTCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGGCTCG[6]CJAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCCAGAGACTGCCTCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGGCTCG[7]CJGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC[6]CJGTGGCTG TGCATATTCCTCCTGCTCCCCAGAGACTGCCTCGCCATCCACAGATGATGGATCTTCAGTGGGT CTCTGGGCTCTAGGCTCGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGCTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTAGTATTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCAATAGCACATCTCCAACTGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATATGTTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAA[7]CJTG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAGTTATTAAGTGTGAAACAAA AATGCCAGAGGATAATATGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC[6]GJTGTTTAAATTAATTCACAATATAAAGTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTCCTTTCTTCTTAAATAAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTAAAGTGAAGGATGGATGTTTCAATAACATAAA GTTCTCTGAATACAACTAAATATATGCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTGCTTTTATAGATTTATGTCCTATGGGATGAGTTTTTAAATGCCACAAGACATAATTA AAATAAATAAATTTGGGAAAAGGTAA[6]GJACAGTAGCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAACTGGAATAAGCCTTCGAAAAGAAATGCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTGCTGATTTTGAACCTGATTCAGGTTAACTGTTCCC CTTGGTATTTGTTAATACCTGTACATAICTTTGAGTTCAAC[7]CTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAGAACGTGCTGTGGGAAGACAAAGTCTGTGGCTTG

WI-19042	193	A C ---			TTTGTCAAGTGTGCTCTCGCAATGCCTCAGTAGCATCTCAGTGTGTGAAGTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAATTTGTGCTCAAGGACATTTGGTGAAGATCCCAACAG ACACAATTTATACTCGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACCAAC/CJGGCTG TGTTAGATTGTAATACTATCTCTTGGACTCTGSAAGAGACCACCTCAAT
WI-18984	208	A C ---			ATTGGCCCTGTACAGTTGCTTATTTATAAATTCATTAAACACTACAGGTGTGAATGGTTAAAA TGTAGGCCCTCCAGTTCATTTTCAGTTATTTCTGAGTGTGCAGACAGCTATTTGCGACTGTATTAAAT GTAACCTATTATGAATCAGAAGCAGTAGACAGATGTTGGTGCATACAAATATTGTGATGCATT TATCTT/CJATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90	T A ---			GCCTCAATTGGCGATTGATTCAGTGCACCAATGTAAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCTTATTGTATTCT/CJATAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76	T C ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT/CJGGGGGTAGCCATTGTGCAGTCAATGGCCCGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-18821a	69	C T ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGGAGGCC A/C/JAGAGGCTGGGGGTAGCCATTGTGCAGTCAATGGCCCGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-19021a	20	C G ---			ACTCCTCTGCTGTCCAT/CJACTGTCTTTGAACAGGAAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGAACAAAGGGTTTATCTAATAAGTGTCTTCCATCAGCTTG CTACCTTACCCACACTTCCCTCTGATTTGGTGAGGACGTGGCATCTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTG
WI-18908	70	G C ---			TGGAAATTCCTTTCATCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG/CJTAGGGAAACATTCATCCTTGAGTCAAAAAATCTCAATTCCTCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155	A G ---			CACGGTTCTCTGCATCGTTACCAGAGCCCTTCTGGTCTAGCCACGCCCTGTATGACCCGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACAC/CJAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACCTGGGGGTGGAAGTGTGGTGCACACAGTGAATGGGAGGTGG
WI-19037a	47	C A ---			CACGGTTCTCTGCATCGTTACCAGAGCCCTTCTGGTCTAGCCACGCCCTGTATGACCCGCAAA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACACAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACCTGGGGGTGGAAGTGTGGTGCACACAGTGAATGGGAGGTGG
WI-19064	66	T C ---			TTGAGGAGGTGGGTGAACCTGCTCCTTGGCAGGGATTTGTGACACTGCATTTGCTGGGTGTTCCT/ CJGGGCTCTTCTGGACCTTGACCCGTGGATACCAGGCCATGTGCCATGGTATTGGGTCTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	---	AGGCCTGTGGCTTATGTCACCAACAGAGGGTCTCTGAGAAGTCTGGCTGGCTGGGATGCCCTGCC CCCTCCTGGAAGGCTCTGACAGATGACTGGGCTGGGAAGCAGAGTCTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACCGACCTACGGCTTCTCTCC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTTAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAAC/C/A/CTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTTGTCTTGCACTGTAG
WI-19016a	161 C T ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTTAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/C/TTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTTGTCTTGCACTGTAG
WI-20096	21 T C ---	---	---	GTTTGGGGCATTTATTCT/C/AGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCGGCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	---	TGGGGCAATTTTAAACACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTCC/C/A/CTACCACTCCCAAGGCAATCTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	---	TGGGGCAATTTTAAACACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTAAAGATTAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTG GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAAGGCAATCTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	---	TCCTCAGCTCTGTCATCCTTGTCTTGGGGTCTGTGTTACGGCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAACATACAAAGCCAGCTCTAGAGGCTCCA/G/A/TCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTGTGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---	---	---	CTCTCCCTAAGGAGCCTTGGCTTGCAGCCCCATTGAGGGATGGAAGTCACAAGACAATGAGT GGAGCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCTGCTCTCCT CCCCAGTCTGTACACTTGGCAAGCAGAGTGGTGGCAGACCCAGCTTGAGAGCTCTGTAGACC GGAAGGAAGGGCGGTCA/T/G/AGGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	---	GACGTGACAAAGGAGGTTAAATGAATCTTTGTTTGT/C/ATGTTCAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACCTTAGGTTAATAAA GGCTATTTGTCCACCACTCTTGGGCTTGTGCAATATCTGGGCTCAAGTGGAGGCCACGTG GGAACAAGGCTCTAGAAAACAAAGGACATGCAAGCTCTCCTGAGCCAGTTCTCT

WI-19766b	93 A G ---				TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAAGTC/G/GJGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTCGGACAAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCACCCCTCCTCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---				TGGCCTCAATGACTGGTACATTGGAGAAGCT/G/ATGGAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTCGGACAAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCACCCCTCCTCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---				CTTCCTCTGTTGGCTTGCATTGTGCGATTGGAAAACCATTGGAAGAGGGACTTTCTCTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTG/C/GJAAAGCTTAGAAAGGAACCTGAATTGCTTCTTTGAATATGGATTTAGGCGGGCGTGGTGGGCTCACGGCTTATTAATCCACGACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---				CTTCCTCTGTTGGCTTGCATTGTGCGATTGGAAAACCATTGGAAGAGGGACTT/GJTCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGCTTAGAAAGGAACCTGAATTGCTTCTTTGAATATGGATTTAGGCGGGCGTGGTGGGCTCACGGCTTATTAATCCACGACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---				GGGCTTAAATCCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCCATAACCCCTTCTACATTGGAAGAGCAGCACACCTTGATACAGATGGTCCGTGAAAGTCTTTTAAACGGACAAAGGTAATACACAGCTAACAAACGATGTTGGCTCAGACGTAACCAACACACCTCTTTTTCAGAACAGAGAGCGTTAAAAGTAAAGGGC/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---				TGTTTGAATAAAATTTCCATGGTCTTAAATTGAAGTGTATGTACTTTCTTTTGAATATCCTTTTTTTCATTAAAATAAT/CJ/TCTAAACCACCTCTATGTTTCAACCTTCTGTTTAACTAAGATATGGGTTTTGGAAAGGCCACAAAGTCACCAGCTCCATGAAGTGGGCGAATGGTCTCTTTTGGAAAGCTCTCAGGGTGTCTCTCCAGAAA
WI-19909a	29 T C ---				CCAGAAATAAGCCTGAATATCTCTT/CJ/TTAAAAATAATTTTCTCTTTCTCTTTCTCTTCCAAATAATCTTAAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGGTTTTTCTCTTATACCTTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---				TTGAGAGGCTGAGAGAAGGCTGTGAGACATTGTAATAAGTCTTAGGGGCATGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTTAGCAGGAGGCAGGAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGGTAAATATTGGGTGACGTCATGCATCCCCCATGCATTGGTTTTG/CJ/ATGCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C	---			TTCTGGTACATGGTAAGTGCTCAGTATTACTAGTGAATGAGCAAGACCTGAAATACTGTCGGA AACAGTAAAAGCAAAATACCACACAATTAGGAGGAATATTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATCAGCAATAATCTATTCATAAACCAAGGTAGATAAATGTCCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCGGTATTT
WI-20895	107	G C	---			TGATGGCAAGTACAAAGGCTCTGAAGAACAGAGTAACAGAGCAGCGAGTGCAGCGTGTGGC CACTCCACAGGAGCAACACTGACTTCATTAAAGGCAAGCGCTTACTCTGTTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCAATCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C	---			CCTGCAATCACAAAGTGGAACTAGTTGATATTTTGAATCATACTTGATTTAACCACTTCAGAAA TTCTATTCJAAAACACTAGCAACTTCCTTTTACAGA
WI-19415c	161	A G	---			CTGGATTTTAATATTCTGGCCTAATAACCAATGTAAATTAATTAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGAAGATTCCCTAAGTAAGGATTTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCATJAGJAAGTCCACCTCATGAAGGAGATGATTCACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCG GCGGTCGATGAAGAGACTGTTGGTCATGGCGGAGCJTGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCCTC
WI-19348b	98	G A	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCG GCGGTCGATGAAGAGACTGTTGGTCATGGCGJAGJTGACGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCCTC
WI-19635	98	A T	---			ATTAGTTCGTGTTGGCCACATTCAAAGCCATCCACACAGCTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTAJATCTTATTGTAGCAGCGGTGTGAGGCTCATTT GTTGAATGAAGCATCCTTAGGCAGCAGTACTGCTGATGCAGATATGTGCTGAAAGAACTTTGCGCTT T
WI-19641a	46	A G	---			TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJAGJATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTTGATTTTGTATTTACAGAAGATGCAGGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A	---			ATATAGATACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCTTCJAGGGTAAACAG GACTATTGCATGAGCATTCCTTAATACGATTTTGTAGGACACAAGTTTCATGCTATTA
WI-19673b	180	C T	---			TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTAATAGT GAAAAGGCAATGATGCTCAGTATCACTGTGAAAACATTTTTCJCTGTTGGACCAAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCGCAAAAAACACAGCCC

WI-19673a	35 G A ---			TCTGCCATGATCACATTGTGATGAAGAACATGATG/GA/JTCACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGATTTACCTACCTGCTTTTGCATCACCAGCTGTAATCTAAT AGTGAAGGCAATGATGTCTCAGTATCACTGTGAAAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCTGAAGGCTTCAAGGTCCACACGTCACAAAACACAGCCC
WI-19724	35 A G ---			TTAATTTGGAAACAAAGGATTGTAATTTGGGTA/A/GJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTTCTCTT
WI-19307	196 T C ---			TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCACAAATGGTACCCCTTCAGCAAGAAGCTG CAAGCCCTTCTTGGATTGCTTCATGAGAAAATGGTGGCTTGGGATGGAGTGACATTCCTTGCTGT GGTGAACCTGCAAAAGAGGAAACACAGGCAATGTATCCATAGAGGCCTTTAAAGAGACCCGTT/CJTTGG AAATGGGCCATGGTCTAATTTGGTTGAATAAATAACCTCTTTGGCTG
WI-19269	85 A T ---			CTTCCCTCATCCCTCTTCCACCACACCATCCCGGAACAGTGTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTGTC/JA/JTTGGGTAGCAATGTGGAACACACAGGCCCTTTGTGGAGAAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTAATTTAGGGCCCTTGGCACCTTGTCTATAGCGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122 C T ---			CAATGGACTGAATGAGTGCCTGCTGGGTGGGTGGGGCACACACCTTCAATACAGTCAAGGTCTG CTTCCAGTTTAGAAAACAGAAATCTGCATCTCAGCTCAGCTGACGACACAGAGGT/C/JTCTTCCCTG ACCCAGAGCACTCAGAGCCAGGTCTGTTTTCAAAACATGCAATTAACCTGGCCAGAGAGTTCAAC CGTAGGCATCTTAATAACTAACTCCAGCAAAATGTTGGGTACGGTTACTAA
WI-19956	141 G A ---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCATAAATAATTATA ATAATATACATCAAGTAACCTTACAGCACACATTTTAAAGGCCAAGTTTGGATCTGTGGACCT CAATGT/GA/JCTCTCGGAGAGGACCCAGTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCAAACAGAGCTTCTGAACCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40 G A ---			TTGGTTGGATACTTGTCTGGAATAAAAAAGCAGTTTAA/JGA/JGTAATCAAAATACCTTTTAAAA GTATTTAGCACAAAGATTTTCTGTAAACTAGATTATGTTGAAACATTTTCTAAATCTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTCTATCCAAATCTATCTTGGCTCTGAAAAACTGCAGA AAGGCACTTGAAAGCTGTTCTTTAAGATAIGGGATTCTTTTATCTT
WI-20218	26 T C ---			CCACACACTCTGGTTTTATAAGCTA/T/CJAGGACAGAGCAGAGTGAACCTGAAAAACAGGGTAG AAAAATAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAGAATGACAAACACCATGTGCCCA GTCAAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 T G ---			CAACCTTTTGGACAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAAATCCCTCTTTTAATATCTCCAGGCTTGATTGGGGAGGGCTGGCTCTACCCCTTCTCTTTCCA TCCAGTCTATTGCCAGAT/GJCCAGAGAAAGCGGGAGGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTCACTCTGTGCTGACTCTCTCATGCTGGGACTGTGCTTTGGGG

WI-20361a	192	G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAATATGTGAATCTGATGTGCCAGAGTTACACTCTGCACCTCCAAGCTA CAACGTGCCACAGCTGAGAGTTTCCCTATACTCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC AAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75	A G ---	---	GAGCCAAACCCAAAACAAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTCTTCTCT TCAGAATT[G/T]CATAAACATCATCTTTTACAACTAGGAGAGCGAGGTAGGCCATAATTGTTCA AATTCATCTTTCTCAAAATTTAAATGTTTAAATCCCAAAGGTGCTATTGAATCTTCAAAAATA AACTGCCATATCAGGTATCATACCTGCAATGCTTCTTAATATCCTTGATTAT
WI-20588	133	G A ---	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAAGAAATGTGAGATCCTTTTGTGGTTTTTATTTCCCTTAAGTACAAAATGCTAAAC G[A]GGAGCCGAGCTCTCCGCATTCAGG
WI-20593	79	A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTCAGTCTGTTG CTGTACTTCAG[G/T]TTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCCCTTCCACCAGACTAT CCAGAGCCATTCATGGGTATTTGGTCTGCACTACTGTGAGACACTGAGCT
WI-19765	57	T C ---	---	TTCTTGCCAAAGCCTGTTCTCAAGTTATTCAGAAGTGGGTGTATACCTTGCTCTCAT[G/C]ATGATCT TGTCCTGCTGCTCTTTAGTTAGCAAGGTGTATGAATACITTTAAGTTTTGTTTCTTTTCCCTCGT GGTATCAGTGAATACTGATCTATCTCTGGTAGGGTCAATTTACAAAATTTGCCATGGAACTGAGC AAAAGGCCACGTGGGATAAAATCACTCACCATCGAGCGCCACCAGTATT
WI-19066i	239	A G ---	---	TGACAAAGGAGAGAAGGGAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACTGG CATATGTTCTTCGTTGGTACCCCTGTAGCTGAATTAATCTCCATATTCGGGATGCTCAATTACAGT ACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTAA
WI-19066g	184	C T ---	---	TGACAAAGGAGAGAAGGGAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACTGG CATATGTTCTTCGTTGGTACCCCTGTAGCTGAATTAATCTCCATATTCGTTGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTAA
WI-19066f	148	T C ---	---	TGACAAAGGAGAGAAGGGAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACTGG CATATGTTCTTCGTTGGTACCCCTGTAGCTGAATTAATCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTAA

WI-19066a	147	G C ---			TGACAAGGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGCTTAGCCAGTCCAATCTCTACGAGGAAGCTGG CATATGTTCTTGCG/GC/JTTGGTCACCCCTGTAGCTGAATTAATCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066c	100	G A ---			TGACAAGGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATC/G/ATJCTTACCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066b	87	C T ---			TGACAAGGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAAC/JTCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066a	72	C T ---			TGACAAGGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/JCTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-20660	105	G C ---			TTTACAGCGAGTTTTCOCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAGAAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTG/GC/JTAAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCGCCCCCAAAATACTGTTTAAACACACTATGTTTAAAGA
WI-18768	120	C T ---			CTGCTGCCAGCTCTCTCTTGCGCCCTGCTCCAGATGGCGGTCTCCTGGCAGCCTCCCGCTCAGTCTCC TCCACCGCCTCTTCTCTCCAGCCTGCCTGCATGCATGTGCACCCCTTGGT/C/JTTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37	A G ---			TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATG/JA/GJATTTAACTTCTAGTTGCTCTTGTCTTG GTCTTCTTCCAAATGATGCTTACTACAGAAAGCAAATCAGACACAATAGAGAAGCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACGGCAACCTGTAAGTCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTGTC/TCTATCTTGCATCTACCTGCTCC
WI-18790	49	A T ---			GAAAGCCAGAGATTAGCCCCGCAATCCGCATCTGCAACCAAGGACAGAA/JTJGSCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTTAAGCAAAGTGATACAAAA CAGTGATTTGGGAATGCCT
WI-18987	35	G A ---			AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC/G/AGTGGCCAGCCAGACACTACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTTAGGCTGGACACAGGATTAGAAAGACACCCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTGCAGCCCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA

WI-18919	26	C T	---			TGGATGAAACACACAGGGATTCCGGA[C/T]GCCAGACCCCAATTTTATACCTTCTACTTCTCTACAGTGTGTTTTGTTGTTGGTTTTATTTTTTATACTTTGGCCATACCACAGAGCTAGATTGCCCAGGTCTGGCTGAATAAA
WI-18741c	64	G A	---			CTTCTGGTCAAGGCTTTGGACATC/TCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A]CTGGAGTTCAGGCTTGAATTAATATAIGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G C	---			CTTCTGGTCAAGGCTTTGGACATC/TCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTTCAGGCTTGAATTAATATAIGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T G	---			CTTCTGGTCAAGGCTTTGGACAT/GTCTTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTTCAGGCTTGAATTAATATAIGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G A	---			TCAGAACGACAGATGGCATCTGTTCCCTGCTTGGTTGGTTGGTGTGTAACCTTTACAGAGACCTGAATTTAGAAATGGCCAGTCTCTATGAGATGGGATATGAGATGGCCTATCGAGATGGCCTATCGCTAACACTGCTGAGTGATTCATAAACATATCAACCA[G/A]TAGCATTAACCCATTTTATTTCTGTCCTTAGTCTGAAGATGCTCACCAGTTTTCTGTGTACAGTAAGGACGATGCT
WI-19212	46	T A	---			CCAAAGTTCATCCATGTTTGATTTCTGATGAGACTAGAGTGACAGT[A/G]TTTCAGAACCCCAATGTCTCAGGTAGTTGGAGCATCTCTATGAGATGGGATATGAGATGGCCTATCGAGATGGCCTATGGAAATGACAGCTGATAATTAAACATTATCAAAAGTCTCTTACAATTTATTTCCGAGCATGTGAGCTAAGTAGACCCATAAGGAGAGAAAAATGCCGTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210	G C	---			CTGTTGAAGGCTTCTCAGGCCAACTCCAGCTTAAAGCCCTAGACAGGTAAAGACACACATTGGATGCGAGCATGGGTTTTCTCCCAATTTATGGGCATGAAATATGTGTTTAGAATAAGGAACAAGCATTATTCCTTGCCAAACAGCCTCACCTAAAGAGGCTTTTGTGTAGTCAAGCAACACACTTGCCTGCTCTGCCCTTGAG[G/C]TGCAATTTGACCTGCTCTCACGTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T C	---			TTGAAATCCAGTCTCTGGCCCCCAGGCGGTCTGTCAACCATAGAATGTCTTCTCTACTGGGGTGTTCTGGCTTTTGTAGAACTTGGCTGAGATGTTCTCCCTGTCCATTAACATTCGATGTTCTTTGTTCAGAGCAATGTTCTGTATTCTGAAACTGAAACTGAACAGATTTGCCCTTTCTCCTAGTCAACC
WI-19041	198	T C	---			AAGCATACTT[C/T]CTCTGGCTCCCAAGTACTTAAATGTTCTCATCTGTGTCTCCCCAGAGTCTCTGACCCCCAGCCCTGTCTGCCCTGTAAAGGGATACAGAGAAGCTCCCCGTCTCTGCATCCCTTCCCAGGGGGTGCCCTTAGTTTGGACATGCTGGTAGCAGACTCAAGGGCGTG
WI-19135	20	G A	---			CACGGTGAGCAGATGAGGCCCAAGCTCATCACACCCAGGGGCCATCCTCTCTCAATACAGCCT[C/G]CCCTTGCAGTCCCTATTTCAAAAATAAAATAGTGTGTCTTGGCTTGGCTGCTGT
WI-19135	20	G A	---			CAGTTACCCCTGCTTTGCCT[G/A]AAGTGTCACTAAATTTGTAAATTTAGTATTAACTCTGTAAGTGTCTGTAGGTACGTTTTATATTATAAAGGACAGACCAAAAAATCAACCTATCAAGGCTTCAAAAACTTTGGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAATGAACGTGATTTTTTATTAAGTGTCTTTGCCATATAAAATGCTGATATTACTGGAAAACTTAGCCAGCTCAG

WI-19236	54	G A	---			TACACAGAGGTCGCACCTTGGACTCTGAGGGTTGGGTGTGGAGGGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCGAGCTTCTCTGTCAGCCGGTTTACATGGGAACAGGGTTTAAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTTCATAGGGGAAGAGTGTACACACTCTGGCTATCTCAGGGGAATGGGGAAAAG AATCTTTCAAGGGCAAAAGAACTCGTGGGAGGATGCTGTGTATGTAACTACT
						GTGCCAGTCTTCAGAAAGCAAGGACTGCCCTTCATTACGCTTGTGACCTCCAGCCTTCTTAAGG CTCAGCCCCACGGGACTCTGTGGCTGCCAGCTTGTAGCTATCTATATATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCAGGAAACCCCTTCTTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTCTGGTG
WI-19144	222	G C	---			CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACACGCTGATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTTGGCAGACACACACTAG[C/A]ATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGAGCTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTCTTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-19139b	110	C A	---			CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACACGCTGATTTACACGAGGGTAGA[C/T]GGCAGATGCCCTGACAGAGAGTGGTTGGCAGACACACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGAGCTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTCTTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T	---			GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGT[G/C]GGCTCATGGCAGAGCATT CAGTCCACCGTTTAGG
WI-18910	112	T C	---			TTCAGGAGGTGGAGTTCGTCAGCTCTCCTGCTGTGATGTGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTGTAGCTTCTCTCACTGCCCGAGTATTGCTCTGTATTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCAATGGTGGAA[G/G]GCTTCATGTATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
	173	A G	---			CGTTTCCCTAACTACCCAGTTTAGTTTGGGATGATTTGATTTCTGTTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAAGT GGCAGCATCCCTCTTCTCCCTAAAGGGACTCTGCGGAAC[C/T]TTTACACACCTCTTCTCAGGGAC GGGCGAGGTGTGTGTGTGTTACACTGAGTGTCCAGAGCAGCACTT
WI-19222	179	C T	---			AAATAATGCAACGAGGAGGAGAAAGAAATGCATTAAGACAAGAACATTCTCATAGAACATTG ATCTGTTTACAGGAAACAAACCTTGCCTTGAAATTACAGCTGAGACTGTACATAATTGCATGAA A[G/G]TAGCTATTTTTCCTTAAGACATTTTTCATTCATGAATATTTCGAAGTTTTCATCTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTG
WI-19117	134	A G	---			

WI-19134c	263 C T ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCTTTACACACTGTCTCCTCTATCTTCCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTCCATCCCAAGCAAGGGGTGCAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAGCAC TTCATCCACTTGCTCCTCCTCTACCTCGGCACCCCTGGGTGGGAAGGG
WI-19134a	162 T C ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCTTTACACACTGTCTCCTCTATCTTCCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTCCATCCCAAGCAAGGGGTGCAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAG CACTTCATCCACTTGCTCCTCCTCTACCTCGGCACCCCTGGGTGGGA
WI-19224	112 C T ---			GGTTTACCAGTCTTCCAGGGAACTCCGATGAAGTGTTCACAAATAAGCGAGTGAAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATATCTTC/TACAGGATGCCTGTGAAGA AAGATCCCTGGATCCCAGGATGATTATAGGACAAAGTTGTTCATAATCCAGCAGGCCAGAAAGACTTCC AGGAAACTCATTCAGGGAGGTGAAAAATGATGGATGACTCCTCCCAAGATGAAAA
WI-19201	179 T C ---			GCAGCTCTAAGGACCACCTGCCATTAGCTCTTGCTTTTGATGGCATCTCTTCCACCTTGCTCTCTC CTTTGCTCCTGTTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACACAGCCTCACACTGCC CTCCGCCCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGAC/TCTGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAAGGTCAGACTCCATGTCTGCTGCTTGGCCTCAA
WI-19034	45 T C ---			GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAAT/CJACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAAAGTTTTACAGTGTTCGTGCTTTGAAAGTGCAATATAAATTTTTTG CTAGCCATGATCAATCGACTTCTATTGTTGATATACACTCAGACTTAAGTTCTGTGCAATTGAC ATTTGCTACTTTATAAACTTAGTCCTAAGTCTTCTATTGCTGTGCTATATA
WI-19102	25 C G ---			TGTTCTGAGTCACGGCTGAGGAGAG/C/GJCTTCACTCAGGAGTTCAGTGATGATCATGAGTTCA TGCGACGTATATTTCCTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATGTTGAGTTTGAAGAAGCTAGAACTCCTGTAAGTTTTGAACCTCAAGGGGAGAAAGTAT AGTGGAAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGACAGAAATGGG
WI-18548b	65 A G ---			AAAGGAGGAGAAATCTTTTTACATAAAATGCCTTGATCATCTCCAGTCCCTCCTCAGTGGGGAA/[A/ G]AAAAAGCATCTNCAAGCTTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---			AAAGGAGGAGAAATCTTTTTACATAAAATGCCTTGATCATCTCCAGTCCCTCCTCAGTGGGG[G/A/A AAAAAAGCATCTNCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---			GGCAGCAGCTTTTTAAATTTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT/CJAAAGATCCAAATTCGAAAGGCCACTGCTGGCTCA CTTCCCTCACA
WI-18501	121 C T ---			CAGAGGGAAGAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCCCTGCAGGACAGAGGGGGC/GCTGGACAGCA GCGCATGCCACAAACATCA

WI-18017	87 C A ---			ACAAAGAAATGGAATAGGTTGGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAATCGTTCAATTAATAATATATCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCCCTTCGATAACCTC/CTTTGGGACTATGAGATCATACCAGATGTGAAACGAAAGCA GTGATTCAGAAACCCNTCGATTCTGAATATCCC/AJGTGGCGCATATGCAAGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTTGTGTGACCACCACTACCAGAGTCAATTTGTAGAGCAGTTAAATCAC/T/C JGCCAAATCCCTCTGCTTCCTTGTAGTCAGTCCTTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCCCTAGACATTT
WI-18265b	117 C A ---			CAATGGGTGGAGTGAATAAAGCATATTGAGAACAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/AJGTTTTCAACCTTTC CTTGGTGGTTCTTCAG
WI-18295	40 C T ---			ACCACACATTTGTGAGAGCCTATTGTGGAGAACAAACAG/C/JTTGGGAAGTAAGGTTGATTACT TCCTCTCCAAGGATGATGTTTAAATGAATCCCTTNCCTTAGCTTTCATTCATATAATGCCAAA
WI-18459b	64 T C ---			GGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAA/T/ CJGAGTAATTACAAACATAATTTTANATGACAGTGCAATTAATTAACTCCTGGGTAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56 A G ---			TTATTTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAAGTGAACAATG/A/GJGAGAAGC AGCAGTGAAGTTTCGGAGAGCGAGGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGAGAAATTTGGC/AJGJCTGTGTAGAATGATTTCTAAAGCTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTGTCTTTGTGTCCTCAGAGGCCTCAGATGGATACGAGCAACTTCCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAG/AJGJGATCCAGCAGTGAGATCAGCAGGTTCTGTGTGCACAGACAG GGAACACAGGC
WI-19888a	98 C T ---			GGCAGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTTATTTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA/C/JTTGGACAACGTTGAAAGATATTAATGCCACT GAACGTTCATTTAAATGGTAATTTTCATGTTATGTGATTTTACCTCAATTAAAGATGGAACATGT CTTATAATTGTAATTACATGAGANCATATTTATGTTGGAAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG/C/JTTGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATGCTTCCACTGCCCAACCAAAAGAAATTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCTGGAGGTTGCATGACAGGATTAGTCTCTGT/T/CJCTTGGT GCAAGTTTGAACCAAGTATTAAGTACCATTCATCAGAGCATCTGTTTCCCTGTCAGATCCCCCACTAG

WI- 20561b	94 T C ---	---	---	CGTTGCTTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC/GGGAAATCAATGCTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAAATGTAA
WI- 20561a	25 A G ---	---	---	CGTTGCTTATTTAAGATGGCTGTTT/GAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATT TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGCTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAAATGTAA
WI- 20116e	69 T A ---	---	---	GCTTTCATTTTCTGTACCCACCCCTGTCCACCAGTTATGTGGCCTTCAATATATGGCGTTAGAACAT A/T/AATAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---	---	---	GCTTTCATTTTCTGTACCCACCCCTGTCCACCAGTTATGTGGCCTTCAATATATGGCGTTAGA CATATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---	---	---	GCTTTCATTTTCTGTACCCAC/C/GCTGTCCACCAGTTATGTGGCCTTCAATATATGGCGTTAGAA CATATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---	---	---	AAAGATTGCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGCACATATTACAAACAG NTCCCAATGGTGAACCTGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAACGGC/ G/ATGTGAACATAATGTTTAAAAAGTTAGAGCTTGTCTCAAGTCAGTCAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTTTATTTCTTGTCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	---	CTGGCAGCAAGTAACCAATTTAAAGAAATACCTCAAC/GAGTCTTTTTTTTATGGGGTATTTC GTTGTTAAACAAAGTTAAATACTTATTGGAACATAATCTTTGTTATTTTTCGAGGAAGAAGAACTCT ATAAGATTGACTTACTCAATTTGACTGGTTTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---	---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTTGAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAAATTAAGTGGTATGG GAGATTGGATAGAT/C/GCCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI- 22091c	205 G A ---	---	---	GGCGTGATTGTGCAATGTCCAACCAAGTCAGCTATCATGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTAACCTCCCTTAAAGTACTCATAATTC ATTACTTGTGTGTAGCTTTTAAAGGTTTAAAAATGTTAGCATTAAGTGGTATTACTTGAGGGCA ACA/G/AAATTACGGCTTAAACAACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45 A T ---	---	---	CAACTGCTGAGGCTTTCACTAGCTGATTTATATCCTATATT/AA/AAAAAAAAATCTATAGTCTG CAGCTTTTGACATCTCTCAAGGGTGGATATGTTGGGAATGCAGACTCCATCAATATGTTGGTT TTGTTGCTTTTGTAGCTTAAGTCTGTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCAATAAATCGAACAGTTGAAGGCTGTTTGTAAATTGCTG
WI- 21778b	155 T C ---	---	---	AAAAATCCATAATTATTGAACCCAAAGTTACAGAGAAAGTTCTGTAACTTTTTATTGAATTTATTGAC TCTGCCGGGTGTCGTTGTCGCTTTCAACTCCAGTCTGTCATGCOOCTGTAGGTGGGTGCCCCAG GTCGGGCTTCTGAGGTCTT/C/GGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	---	TGAGTCAGTGGTCAGATGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCTCT CAAATGATCTAGAGCTATCCTTGGCGTACATGAGGGCAGTTGTTCTAGTACCCATTAGCCC ATGGCTCTCAAGCCAAATCACACTGGGAAACACACCCCTCACAGATGCCCTATCCATTGAGTTC ATACAGGTTTTAGTAGCTAGACTAGAAACATTTTTTA/C/AAATTATCTA
WI- 21449b	222 C T ---	---	---	AACAGCAGCAGTCACCTCCAAATGCAAAAAAATTAACAATTTTAGAATAAAATTAATGTTTA TAATGCGGGTCAGAGANTTGAAGGTACACAGAAATCAATCAGCAGCTGGAGCGGTGGAG AAGCCAAAGCCCACTGTGTCAGGGTCCAAAGCTGACAAGAAAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/C/TTGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	---	GCCTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAAACCGACTCCAGCTGGAAAACTGCCCTC CCATCCCCCTTAGCGCTTCTGGCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI- 22187b	178 G A ---	---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCATGGGTGATTACATTTAAAAACCAAAACCAAAACAAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGTAATGGTG/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 22187a	110 C A ---	---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGTAATGGTGAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 21609b	146 G A ---	---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTTAACAACAGTGCAGTCCGTTACAAGCTGTAAA AACAGCCCCAAACCAAGACATCACAGAGCAAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG/AJAGGGTCCCGGCTATGTGGCCACTGTGATGTAGGCAGTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAACAA/C/TGTGCAGTCCGTTTCAAGCTGT AAAAAAGCCCAACCCAAAGACATCACAAGAGGAAGAGCAGTGGCAGTGAGAAAGGAGCCTGTA AAGGATGTTTCAAAGGAGGTCCTGGCTATGTGGCCACTGGATGAGGCAGTGAAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCTCCCTAGGGCTTCA GGGTAGCCCTGACATCATGGTCTTTTGATCTGTG/JACCTCACCCATGCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGG/C/TATGTGACAG TTTC/JGTGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGG/C/TATGTGACAG GGTTTCATGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATACTTATGTACTTCTTG/JGTTC TCATACAAGACAAAGCACAAAAGCACCACCCATGCCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG/JAATAACTTATGTACTTCTTGATTCTCA TCATACAAGACAAAGCACAAAAGCACCACCCATGCCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCCAAAAAATTTCTTAATATAGTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/G/JGACACAAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTACTAAGATTAGATGAACACACACTCAGAAATCTCTAGGAGAGCTGAAAAGAAAGGAAC AGATGTTAACAAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACCTAAAGGCCGTGAAGGCATGATTGTTTGGCACACAGAGTGGATAACCAIT/JACAT TGGCTGGAATGAGGTGTCAGGAAATAAANTGCAACAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAGAGCTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCACCATCACCAGCCCTGCCCATCATGCATCCATGATTACTAGCAGTAGGAA GCCAAGGGAANAGGACCCCGCGCTTGCT/C/JGTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGAGGTTACATGGTCTCATGCACTGCCCTGTGATGGGAATGAC

WI-21661	117 G C	---	---	GCCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAAG/GCJTTAGTCACAGTC ACACAAAACCTACCTTCTAAGGAAAACCTGCCAGTGAAGCCGTAAATTTGTCTTCAGCTATGAAG GA
WI-21980a	25 T C	---	---	TCAGTTAAACACATTCATCAAGGAT/CJAGATTAAATTAATGTGAGGTGAGCATAAAAGGGAGATTAA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTCAAGTGACTCAGGATAAGTTTATTAAATTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G	---	---	TGCTTGATTAAATGTGGTGTACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTTT AAA/A/GJTAGCAATATCTATTATAATAAATTTGAAATAACACCATATAATATCATAAGGA AGTAATCTAATGTGTGATTTCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 G A	---	---	TTGCTATAATTTCTTAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAACTCACTATTAGA CAAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACAG/AJGAGTTAATTAACATAAG GAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTCTGGGGCC AAAACCCACTGAACCTACCCAGCTGAAACACACTGAAGGATCTGGGTAAAGGA
WI-21524b	97 C T	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGACGACCTTCGGCTACACTTAT AATGGTTAATAACAGCATTCCTGTCTACCC/CJGATGATGCTTCTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCCTCCAGGGGATG
WI-21524a	35 A C	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT/AJGSCCTGATGACGACCTTCGGCTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCCTCCAGGGGATG
WI-22652a	32 G T	---	---	TTACCTTCCAAAACCCAGGCCACTTTGGAGAAA/GJGAGAGAAATGCTATTAAATCAATAAGCCAAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACCATCATTCCTGCCACAGAACC TTTGACATGCTGCCCTCCCTACTCCGCACCTCACCTGCTTAATTTGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197 A G	---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGGAGGGCTC TGCATCCCTTTCTCAGCAGACAGCACCCTCTCACCTCTCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGCTTTTCTCACCAGGGTAAGAAATGCAGGTTATTGCAGAGGGGAGTGAGTCTGGGA/A/GJG TGGGCAGAGCAGCTAGGGCAAGGACTTAAGGGAACCTTGTTGGGGGAAGAG

WI-21703c	134 A G ---			CAACAGGCTCATGGAACAGAGCCTAGGATCCAGGAGCATAGGAGGTGGTGGTGGGAGGGCTC TGCATCCCTTTCTCAGCAGCAGCATCTTCAACCCTCTCTGGAAAGCAGCATTTGGAGCCTACACQ A/GCTTGTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG TGGCAGAGCAGCAGTAGGGGCAAGGACTTAAGGAACCTTGTGGGGGAAGAG
WI-22663c	139 G A ---			CCCTTGTCAGTGTGCTCGGCTTCTACTGCACTGGCGAGGTGAGCCGGCTCGCTAATCTTATTTC CCAGTCTGGTGAACATGGGTGAGTCTCTCCCGGCTCAGTGTGGGTTTGCACGTGTGCACCTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTCTCTGAATCCCGTGTGAATGTGGGT
WI-22663b	55 C T ---			CCCTTGTCAGTGTGCTCGGCTTCTACTGCACTGGGAGGTGAGCCGGCTC/GTGC7AATCTTA TTCCAGTCTGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTAC AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTCTGAATCCCGTGTGAATGTGGGT
WI-22663a	38 C T ---			CCCTTGTCAGTGTGCTCGGCTTCTACTGCACTGGTGAAGCCGGCTCGCTAATCTTA TTCCAGTCTGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTAC AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTCTGAATCCCGTGTGAATGTGGGT
WI-22668	99 A G ---			TCCTTTATCTGCTGCCTGCCTGAGTATCTGGGAATCTCAAGGATTTGAGGAGCCCTTGGGATT CCAACCTAAACAAATTAGTTTTCTGTAATATTA/GJTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAAACCAATTAATATCAAAAGTATAACAGCAATTTAAGTCAGCTTTTCGAAGAAACCTTTATT
WI-22631a	52 T C ---			AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCTGGCTTCAGTCTGAT/GJAGCACCACTTT CAAGTTTTAGGCAAGGATTTAACTCTCAGGCTCATTTCTCTTTTGTAAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTTGGACAAATCAACTGAAATTTTT
WI-20258	157 G T ---			AATCCACACTTTCACGGAGGGGACCAGCCTGCCATGTCTGTCGCCAGGCTCACAGAGCGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCCGTAAGGCATGACAACG GGAGCCCGCGGGGTGTTTCAG/GTJCGGTTGACGAGGTGCATGGCTGGCAGGGCGGCTCTACAGA AGGAGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTACC
WI-22714	212 C A ---			ACTACACATATGCTGATTTCAACAGTAAGAAATTAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTGTTTCCACTCTCCCTGCTAAGTGTGACAGGAGTGTGTGGGAAACGAAGT CTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCTCTGTAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/CJA/TGAGTAGGGGCCAAACATCTTAAACAGCTAGTTGCT
WI-22734a	44 G A ---			TGGGGCTACTTTAGATGGGATGGCGTCAAGGCTCTGGGAAGGCCT/GA/TCTTAGAAGACATTACCCA AATGATGAGAGCAGCCAGTCTGTCGAAGCCATAGTTTGGATGGCAGACTTTTCCGGCAGAGGAAAT AGCAAGTGCAAAGGCCCTGAGGGAGAAATGAATCTGGGCTTGTCTCTACAGGTTGAAGGCGGCCGCT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A G ---				TGATATGATGTCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAAGAGTGTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACCTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAAT
WI-22750	48	G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAATG[A/G]GCTCATACAAAGGT TTGGAAGACCAATCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTCTGACTGTGCT
WI-22775a	60	A G ---				TGCTGTTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTCCTTCCATTTGTTACATC[A/G]TAGTA GGAAAGGGAAATAAATCCCTAAGGGCAGCAATAATTTCTGCTTTTGAATCCTTCATTTCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C T ---				CTTAGCTAATAAGAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCTCTGTGTCTTGAGCCCTCATCCCAACCCCTCCAGCCCTCATGCCCAACACACCCGTGTCACCAATT CCCCATCTCCCTGTCTGCTCCCATCTCAAGTCCAATTCOAAGGCCAGAGCCCTGGAGCTTTTCTG GGAGACAGCATGAAAGAGGGGAGTGAGATGGCAGAGATGGGTGGAGCCAGTGCCTGTGGGTC CTG[A/T]TGGCGTGGTGTGTGGGGCCCAATCCTGAGGCCAGAGGTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCAATTTGTCTCCACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122	A T ---				CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTATGGGTTCACTTATATATCCTTTATCACTAT GACTTTCATTGATTTTATTTATTTGTTCTCCATTTCTCTGCAAACTTTTC[A/T]TTTGTATATAA ACTGTTTCTAACTTCACCTTAATCTCTATCTGTTTCTGTTTCTGAGTTCCTGAACTTCTTTAGAGG
WI-21186	95	G A ---				AGCAGCATCAGAAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCCAAGAGCTTCT GATTTCAGTAGGCTGAGGTGGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCCTAAGTGTTCAG ATGCTGCTTGTCGCCGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTCTTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATATGTTATGAAT
WI-21187a	94	A G ---				CCACGATAACTATAAAGCAGAAATTAGCTTTGAAATCAAAATACATATTTAGTAACACACACATT CATTTTATAAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCAATTTGCATCACCTAGGGGAATGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAGCAACCTGT

WI-21190	39 T C ---	---	TTTCCCCACATACCAATGCACCTGTTTGATATAAACTATTTGCTGGGGTAAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATTTATAACAAATAATTTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTTTATTGAGAAAGGAGAAGTCAGCATAGTTTATTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186 GA ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATACTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTCGATGCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 CT ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATACTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTCGATGCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 CT ---	---	GAAAACGGGGTGTAAACAAGAAAGTCTCAGATCCCACCTGAAATCTGTTCAAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTCCTGGGG TCCAATCACATACCTCAGGTTCCAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANITAGCAGT CCTCTCATTTCTACAGTCTGTATTTCTTCTACTGAATCTTGGTGGGAG
WI-21122a	42 CT ---	---	TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCATC/TTTAACAGGAACTCTGTTTTCC TTATTCAAATGTCACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGACAACTGGAAATACT AAACAATACTGGAAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGCCTATTTGTGGTGTCT
WI-21254	53 A G ---	---	CAGTTTGTACAGGAAGGGCCCATGAATGTGGGCGGAACCTATCCACAGGAG/GGCAAGGAGAAG CTGTTCTCTGG
WI-21054	23 GT ---	---	AAGGAACTGCATGGGTACAAATG/TTCCAATTTCATACTTAAACAGGTGGGAAACGGGTCAATCT TGGCTGCTCCAGAACAAAGGGCGAGTCTATGCACCTCTG
WI-21059b	181 TC ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACCTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCCAGCTTCGTACATCTTAATTCAGCTGAAA AATCCTGGGGAAGAGACATACCTCACTGAAGTCAATTCCTATTC/T/CJATTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 CT ---	---	GGGACCAGGGTAACACCATAGCAATATCCGTTATCAGCCTTATCTTCCCACCTGAGCCTGGC/TJT GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCCAGCTTCGTACATCTTAATTCAGCTG AAAAATCCTGGGGAAGAGACATACCTCACTGAAGTCAATTCCTATTCATTTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-20442	37 T C ---	---	TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAGGTGGCACAATTTTAAGAAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43 T C ---	---	GTGACAAGAGGTGAAGCAAGGGACAGGGGCAGCGAGT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---	---	ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTA ATCAACGTTAAATTTTGCCGACCAGTTCTTCATTGCTGATCACTTTTGATAATGACAGATCCAACAT GAACTCCTGAAGCAAAATGAATATTACCTTGCTTTTCAATGCAAAATTTAGGACCAAACTCAAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGACAGGGATCTCT
WI-21149a	167 G A ---	---	AGGACCTGCTCACACGTTCCCTCACCCACCAGCTTTTGGCAAGATGTTGACTAAATACCCT AAATAGTGGCTTTTATTTTAAACATGACCTTATTTATCTTTTAACTTAACTGAGTCTTATATA CAGACCTGCCCACTGGAAAGCTTTTACACGATGCTTCAGAAATCGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---	---	GGTGCAACTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGTCCTCGGTGAACCA GACAGTGTGAATCTGTTCCAGCCCAAACTGACAGCAATAGGGATGAGTTCTC/WGJGAAGTGATTCT GAACTGAGCACGCACTCATGCTGCTGAGGGGAAGTCTGGGGAAGAGCCT
WI-21382d	125 C G ---	---	CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGAGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAAGTGGGGGGGTTTGGATCCAGTGGGATNTGGCTTCOC/CJAGGTT GCAACCCAAAGGAAGTCTCTGGAAGCAGCACCAAGTCTGATGGGGAGAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---	---	TCCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAGAGGGACAAGGGGTCAGGGGCGAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCCTTTGGGATGGAAGTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCGAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGGTACCTTTACAGGGGCG /AJCAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCTGGGAACAGT
WI-21202b	156 A C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTATGAACATGTTATTTTATAAAATGGTCACAATATATTTTAACTGATTATTTAGGGG AGGAGGAGAGAGTTGACCAAJCJGTCTACATGATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATGA TCTGTTTATGAACATGTTATTTTATAAAATGGTCACAATATATTTTAACTGATTATTTGA GGGAGGAGGAGAGTTGACCAAAAGTCTACATGATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATAATTAACCATATTTTACATAATTTGTAGG GACAGTACTATACTCTACAAATAAAGGGTTTAAAAATGTGTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAACCATATTTTACATAATTTGTAGG GACAGTACTATACTCTACAAATAAAGGGTTTAAAAATGTGTGCTTA
WI-21399a	75 C T ---	---	GGATTGAGTCCCAACTGATCTCAAAATTCACCTTCTTGCAATGTAACAAGCTCATTCCTCTCTAAAGTT TCAGTT[C/T]TTCACCAAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTTCTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI-20328a	68 G A ---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGAGTGGGTCACAGACAAAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAAAACAGTAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATTCAAATGTACATGTAATAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACCT TAGTATCTAAGTATCCAATCACAATTGATCTAAGTTTTCACTTTTAAGAAACATTATAAAGGTAATT AAAACTCTAGGTGTATACCTTA[T/C]ATGGAACCTAGTTTATTTCCNATTTAACTACTGTTTCATTTGGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAATTATAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGGCCATTAGAAAAATAAGAGCCAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTAACAGTGGGGCAGGGCCGTTCCGCTCCAGCTGGGTTTCCCC AGATGCAACAAT[C/T]GGGGTTCTGGCTTCTCCACTGGTGGGATCGCGCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGTGTT CTCTATGGACCGAGGCCCTGAAACGCGGGCAGGGAGGGGCAGAGAA[C/G/A]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCATTGCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACCTGGGCTGCTTTGGAGAAGGCA[A/G]AAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCCTATTTCCTCCCTGAAG

WI- 21514b	133	C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAGGAGCACAATTACCATGGAGC/C /TACAGGACTCGAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGCAAGGGTCATAAGGAACT
WI- 21514a	100	A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCA/A/GTCTTCAAGGAAGGAGCACAATTACCATGGA GCCACAGGACTCGAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGCAAGGGTCATAAGGAACT
WI-22020	27	C G ---	---	ATGAACATGTTGCAGTGGGATGAATC/GTTCATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGTATCATTTCTACCTGTATGAGGGTACTT
WI- 19576a	113	A G ---	---	TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAAACATTC/GTCTAGTTCAGTGATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA G
WI- 21695a	141	A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAGGCAGTGGCACTTGGAAAGTCACTACACATGGCAATA AGCAGCCTATCTCTTACCACCAAGAGTTCTTGGGSCATGTGATGGTAGGCCAGACCCCTTTCCAA GGGAATA/CJ/ACTACACTAAGCCTACACTGTACTGTGAGAGTCTAGTGGTGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCCCAGCAT
WI- 21574a	235	C T ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACCTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTACTGCCTACTTCC/TJ/TJCTGTCTCAGGTGGGA
WI- 21644c	151	T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTCTAACCTTTACGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTCCACCATANTATTTAACAGACTCAAAGTGATACATAACAAGCTTG TTTCATAAATAAGGGA/TJ/TJCAATCAAGATCCATGGAATGATGCAGTTTAAACATGTGTCTCAGC TTGCCTACTGACCACCTTTCCCTTTCTAAATATGGCAACAGCAGCAAGTC
WI- 21614b	55	G A ---	---	TGCTTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANTATAGCTATC/GA/JTTTAAACA AACCTCATATGATCACTGTTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGTATTCTAAGGTACTAGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAAGTTGGCTGTGTGGG
WI- 21615b	151	C T ---	---	GACCGAGAAAAAAGTGCAGGCATATGATGTTTGTGGAAGTACATGACTATTTCAGCTTATAGA GAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATATTAAGATAAGGATGGACT CTTTCAGTGAGTATT/CJ/TJAGGACACAATCGACGGATGTAATCTATTGANTTATACCATAGGCC TATTCTATATTGGGCCAAAGGGGAAAGGTAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAAATCATAGATGGCAGAAATACATATTTCTTGAAGAAAAAAATTA[AGT CTCCCTTATGGTACTGTGATTTCATAGGGTGTGGGTAAGTACATGACAACATGCATGGGATAGA CACTGTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCCTCTCAGTATTTAGATGAGGATAGAACAGATAGCGGTGTAACAGCCCTCTCCACTGCT TACTGTGTGTACCAAGAGGCGAGAAAGCAGCTACCCCAAGCCTAACCTGGCC[C/T]GTCTTTTTCAG GCTTCTCAGGATGCCACAGACATACTGGGGAACCTGGGATGCAGGGAGAGCCAGGGTCTGTCTTC AGGAGGGTACAGC
WI-19105c	211 C T ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAAATATTTGTGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTCCCC ACAACTTC[CT]TCCAGGGGCAGGATTTCCACCCAGGGCCCAAGGGTCCCCG
WI-19105a	33 T C ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAAATATTT[CT]GTGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTTGTCTGAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCAGTGGATCTC CCCACAACTTCTCTCCAGGGGCAGGATTTCCACCCAGGGCCCAAGGGTCCCCG
WI-21760c	81 C A ---	---	CAAACTAGTCACTACTGATGCAAAATGATTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[CA]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTAGTCACTACTGATGCAAAATGATTGG[AG]GGGTCTTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTTGCCAGCACCACTATTACTGTTATTTCTCTTTGAGGAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCTTAACTATGTTAAATCCTTTTCTTACCAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTACT[TC] AGAGACAATTCATAGTTTCATATCTTTCAGGGTTGTCTTACTTGGGGGGC
WI-20934a	72 T G ---	---	CCAACTGCAACATAGTCTTCTATTCTTAAAGTACATAGTAAGGTATGAAAAACATTTGTATTCA GAGAA[TT]GTCTAAGACAAATGGTCAAAATTTCAAAATGGCCTGGCACTAGTGGTAATTCAGCAGAC AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAAATACGTGCCCAATTGCAATGAGTTACCCAATC AAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAGACCCCTTTCACAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAACCTT[GT]CCTTTAAC CTCTCCAGGCAAGAAAGGAAAGTATGATCATATTGATTTCTCAGAAATGGTGGATCTCAAGACTT TTTAGAAAGTGTCTTAAAGTATAAGAGGCTTGAATATATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAGAAATTTTGGATGCATTTGCCCCA

[illegible]

WI- 22082b	67	CT ---	---	CAGGACTTGGTTGCTGTCCAACTGCACATAAATGTCCCTTTTGTGTTAGTTATGGTTGTGTGIC /TGTTTTCTTTTGCATAAGAAATATGTCATTATAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGTACACGGGGCTCGCTAGTCCGCGGAGGAGGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAAATCCTCTTTGCTGCAACCTCT
WI-20993	139	A G ---	---	AACACAAACTCCATGCTTCAAGATTCCCACACCCAGATACTAAGACATATTAAAAATTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCTA/GTAAACAAAGTGAGTATACATTAAGACAGTATTGCAAGATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCATTTCAGGTCTCCTAGCTCATCCACACACATCACC
WI- 21723b	125	A G ---	---	AAGCGATTTTATTAATTTGATTGGACATACTGTAGGTCAAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAAG/GJCAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI- 21723a	82	G A ---	---	AAGCGATTTTATTAATTTGATTGGACATACTGTAGGTCAAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTG/GJACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T G ---	---	CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTTT/GJCCCCATTCTCTAATCTCTTTTGCCTTACAA TATATTACCTTCTAGGTATCACTCATCTATAGGAATGCCCTCTAGTTTAAATGCTCCTGCCCAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTAAATGGGACAGTGGG
WI- 21006a	106	A G ---	---	TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACATGTGCACACAC/GJAGAGGCAAGTACAAAAATGTAACC CCACAAAGTGCATGTGAATGAAGTGCAAAAAGGCTTCATTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAATAACAGAAAGGCTCTAACTGCCCTAGGCCT
WI- 21761b	138	C G ---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCCTGGCTTGGAAATAACTGAAAGATTCTAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTTCTCTGCTGCCAGTTAAACGTGCCGTGG CT/GJCAATACACACCAAGCCAAAGCGTAACTTGGCTGCCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI- 21079c	166	G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGTCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGAGCTTTGATTCCTCCATGAAATTAAGCTGTGTTGCTCACTTGTTTACATAA CTCAGGCCACCGTGAATATCTGTAGTGGG/GJAAATTTACAACCACTGACCATCTCAGCTCAAA GCCAGATGACTATCCTACATCTGCCAGGGTAATAGGCATGGGCAAT

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WI-21079a	50 G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCACTGTGTG[AJCGCAAAATCAAGT TGTTTAAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCAGTTGTACAA TAACTAGGCCACCTGAAATATCTGCTAGTGGGAATTTACAAACCAGTACCACCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGATGGCAAT
WI-22129a	45 T G ---	---	TCGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAGT[GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGCAATAAGTTAGCTCTAACAGTTAAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAATAATAATAATTTGGTGCAAATCCAGNAAAGGCA TTAACCAACATGGGACTGATCCTGGGGCTTCCACCTGACTAAGTTTAA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC[A/GJGGATGAGGCTCTTCTGTAAGTCCAAACAGACGCTCACAGTGTGGAGGCT GGGACTGCCAGGTTGGAGCTCACCCAGAGAGGCTCAGTGCATTTGACCCCAACCCACCTCACC CAGCACACAGGCACACGAGGGCACACGCACACACGNTGCACCTCACCACGC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTGATACCAACATCTTACAGCAGCTCAGC[GJTGCGTTCCCACTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTGATACCAACATCTTACAGCAGCTCAGC[GJTGCGTTCCCACTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTAGCTGTAGCCTAGTCCAGGNTCTTGGCCCCAATTTCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCTGACCCCTCACCACCCCAAAAT[A/G JCTTTTAACTCTGGAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACTTAGGGACACCAGCCCTGGCCCTGCCCT[GJTAGCTGCATGCCACCTC ATATCCACCCCATCCCAAGCTCTCTGCCCGACACCCCAAGGCTCCCTGCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTCTTGATCCCAACCACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAGCCCTAGCATAAAATAGCTAAGTAAATGTTTCCAAAGATG[C/GJCTGCATCAGTAT CTCCCATCCACATATTTCTGTTGATTTGCCATCACCACIAAAATGGTGGGATCTACCTCCCT CCTTGCAAAATTTGAGCTGNNCCTCTGATCCTGCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTTTACCTCTGGCTTTACAGTAGGCTTTGGCTAATGGCCANTGAACACTGCAGGGCAAG AGGAGTGAGGGG[C/JTACAGCAATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACTATTCG

WI-19891c	172 C G ---	---	TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAATTCGTTGGTGGCCCTCCCTCCCTCCCG ACTCCTCTGTCCTGGGAAACGTGGCTTGNCTCCAGACACAGTGTGAGATGCCAGCTCTCCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGCTGACTC/GC/GCTCTCCCGGGCGTGGGCGTGTCTGT CAGGCAGGGCGGGGAGGAAGGAAGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---	---	GCACCTGTAGGGGTGTAGCTTCCATGGTTCTCCAAGCACGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGC/TJGCAAACTGCTTTGAGGAAATNCCCCAGGAGGAATAAAGTAGAAGACGC ACCTGCTATTTACCATACTATGGAGAAATACAGCTAATGAAGTGGTGGCAGAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTCTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGGCTAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/TJGACACAGGATTTATACACGGTGGCAGCGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGGGAGGCGAGGNGGGTGGGAA
WI-20270a	53 G A ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGGC/GA/JTCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACAGGATTTATACAGGTGGCAGCGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGGGAGGCGAGGNGGGTGGGAA
WI-20622	130 T C ---	---	CCACTTTCATAATTTTACAAAATGCTCAGCGAGCAAAATATGAAAAGCTTCAACACTTTCCTTTGTGTA ACTTGTGCAATAAATGCAACTTTAACAAACATACAAAATTTCTCTGTATCTTAAAGTTGAA/T/C/ TACTAAATTTTATGATGTACTCATATTTTATTCATATACATCTTTAATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCAACTCTGTCATGCAG
WI-20768b	190 C T ---	---	TCCCACTCAAAACTCCCAACCTTCTCTGGAAGGCGGGCTAACAGGACCTCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCAATTCGTATATCACCACTTA CAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGTGGGA/C/TJGAGGGACTC GTAATTCGCCCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	TCCCACTCAAAACTCCCAACCTTCTCTGGAAGGCGGGCTAACAGGACCTCTGCCTGCCTGC TCA/C/TJGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCAATTCGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGTGGGACCAAGGACTC GTAATTCGCCCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAATATCTCATCTGTGCACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTTGGTCATCTTTAAAGAAA TGCTTTAACATACCAAAG/A/TJAGTGGAAATCAATAGAATAAATAATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATAGGATACCCTAAATTTATTTCTATGTATGGAAAG

WI-22202	128	A G ---	---		TGTTGCTTTGGTTGTTGCTTTCTGGAACATATTGGAACACTTGTCTTTCATTAAGCTGCTCAGACGT GGCACAATCCCATCCATCTTCAGGCTTTTAAATAGGTCATTATGAATCTGAATTTCTT[A/G]TTAAT ACTCTGGTGCATTCATTTCATCTGCAAAAGCAACTGGCACAACACTCTCTTCCCGGTGCAGCTCTCGG AGAACATCTAAATTAGTCTAGTTCTGTGCGGAACITTCACAGCTCAC
WI-22189	70	C T ---	---		CCAAGGATGAAATTCACATTTATTTTNCITTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AACTGAGGCGAGGAATGGCATGGGCTGGGCTGGGTACGAGCTGGACGTTGTCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109	T C ---	---		GGGAGGCATCATAGAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCTCTGCAAGCTCTGGTTGT[C]TTTCATTTGCAAAATAAAACCCA GACCGGTCATCTTTTCAGTTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGATGATTTATCAGTCTCCCTGATGCACCTCAACTCCAATGATGCAAAAG
WI-22290a	136	C T ---	---		GACGTATCTCTGAGGCTCTGCCAGTGGATTAGGTGAAGAGAGGTTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCATGCAATGGTGAGTGGGATCTGGGGGGTGCAGGACCTTGTCTTT [C/T]TCCAATCTCTCTTTCAGCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCTTTTCCCAAATGTGTAAGGTCCCAATCCAGACCCCTCCAG
WI-22292	53	A G ---	---		CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA[A/G]GTTTGTAGTAC GGTCGTTTAAAAAATACTTATCTGACACAGTGGAA
WI-22387	186	C T ---	---		ACCTTGACACCTGCCATCCGGTGCCATCTCTGGCTGGCACATCTATACCCACTCTGGCTCGAAAG GCTTGTCAACCAAAATGGCAGCTGGGCTAAGGCTAAGGCTATTAAACAAAGGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCTCAGCAAGGCGAGGATTGTGGT[C/T]CCTTGTGTTTCTG AACAGGGCCCGAGGCGAGCAAGGCATGCCATCACTGCAGCACTCAAGCCCT
WI-22395b	127	A G ---	---		GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAGGGGGCAACTCTTTAAT[A/G]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90	A C ---	---		TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTTCTCAGTG
WI-22419b	67	T C ---	---		CCCTTCTGGACAGTTTGTCTTATGTGTTACAGACAATCAAGGNTCCCTTCCAGGCACAGCCCAGTGC[T] [C]CTGGATGGCATCAGCACAGGCTCCCTGCCCGGCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59	T C ---	---		ATTTTCCCTTTCTGTGTTGTTGTTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT[C]TGGAA ATCTGCATGATTAAATAACATTAAAGTTTCAATACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATTCACATTCTCCTCCTAGTT T

WI- 21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTGAGCAGACATTGCCTGTGCTTCTACCCACAGCAGCTGCTAGTGCACTT GA
WI- 21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT T/CJGCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCACAGCAGCTGCTAGTGCACTT GA
WI-22440	64 A C ---	---	CAGTCCATTGAGTCCCAAGTCGAGGGTGCACTTCTCCTTTATCTTGCTTAAGCCACTTGGGTAA/CJ TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAAGTCCCTGGAGGGAGGAGGCTTTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAG TTCTTTT/CJGAAAAAATACACAATGGGAACGTGACA
WI- 21965a	112 A G ---	---	CAGGTTCCACAGAGGCTTTATTTACGCCACTCAGGACCCCTGGCTTCTGCTCCAAGGCACCTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCJ/GJCCCCACAGGGTCTCTGT TCCCAAGTCCTGATGATTGAGCAAGACCTTACACATTACCCACTACCTGCTGGAGAGGAGGCTC ATGAGGCAGCCTGTGGTGCOCAGCTCAGTGTGACACACTGCCAATGTGC
WI- 21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTCAAGTTCA AACCACATGGTTTCTTAGTCAGAAAGTCTCATGGACTTCTCCTAAGCJ/GJTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI- 22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTTCAAACTATTGACTATACAGAG TCTTCAATTTCCAAAAACAGTTAATAGTAACTTGGTGGCACATACAAATGCATTGAATCTGTAT TATTCAGTAACTAAAT/CJAGGNTCTGCATCATTTCTCTTACA
WI- 22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAACAATAAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATGGGTTATTATGGGTCTCTGCCTCTGGCTGTGTTATGCT GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI- 22250a	89 G A ---	---	ACTTGTCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAACAATAAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATGGGTTATTATGGGTCTCTGCCTCTGGCTGTGTTATGCT GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR- 04932-2b	192 G C ---	---	GCAGCCATCTCTCTCCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTAGTGGCCCGAGTACGACCCGCCCTGGCCCCAGGTTCTCGGCTCTCAGGACGTCOCAGCAAGTGA GCCAGAGGTTTCTGTGGGACTCCAGCCAGGGGATGAGCCCGCAGCCCAACCTG/CJAGTGTCTC TTTGACGGGGCCCGCTGCTCAGTCTGCTCTGAGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149	C T ---	---	GCAGCATCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCCCAGCAGCAC CTAGTGGCCCGAGTACGACCCCGCTGGCCCCAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGGA GCCAGAGGTTTC/TTGGGACTCCAGCCAGGGGATAGGCCAGCCCAAGACCTGGAGTGCTTC TTTGACGGGGCCCGTCTCAGCTCTCTGGAGGTGAGGAAGGAGGT
stFIBBb	412	G C ---	---	GTGAGGAAGATGGAACCTGGACAGAGTCAAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCACCTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACCGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGTTACGATGGTCTGAGCTCTCTAGAACCTTCCATGGTT
stFIBBa	341	T C ---	---	GTGAGGAAGATGGAACCTGGACAGAGTCAAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCACCTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACCGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCATCTGTTACGATGGTCTGAGCTCTCTAGAACCTTCCATGGTT
stGLV2	61	T C ---	---	GTCAAGAGGACGGCTCTGGGACGTCTCCACCATGGCTGGCTGCTGCTCCTCACTC/CTCTC CTCACTCAGGACACAGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTC TCCTGCTCCTAGGCTCACCGGGGCCAGCACTGACTCACTGGCATGT
stSG1001 7c	70	T C ---	---	GTTCAAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGGAT TA/TCJAGGCATGAGCCCCACACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTTAATCC
stSG1001 7a	33	G A ---	---	GTTCAAGGCTCATCTTGAACCTCTGGTGTCAAGC/TAATCCTCCACCTCGACCTCCAGGGTGTGG GATTATAGGCATGAGCCCCACACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTTAATCC
stSG1002 3	63	A T ---	---	TAATGATAATTAGGCACTTCTCCACACGAAGATGACACAATTGACCCCAATATCATTTGAGGC/A/T AACAGTTTGGGCTGTTTTCAGTAGTATGACAGTGA
stSG1009 6	36	G C ---	---	GTGGAGAAAGATCGTCTTCTCTCCCTCCCATGAC/CTGGCTTCCCGGGGCACTGTGCGTTTCC ACCCGAGACGGCCTTTGAGGGACCCACTGCCACTCCGCTGTGCGTGGTTOGGCCTCTAG GGCTCGAGTGTTAAG
stSG1011 8	107	C A ---	---	TAGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGGCTGAGGGGAGTACCCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATTCCTTGGC/TA/CTCAGCCCTCAGTCTCTCAATTTCC ACCAGGCCGTGCTTGTGAGTTTCTCCAGTGA
stSG1012 0	89	T C ---	---	TAGTAGTAAGAAAGCAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTCAGAACACTTTAAT/AT/CTGTGTGTAATCTGATTTATCCTGCTTACAAATG
stSG1017 8	42	C T ---	---	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG/CTGGGAGGAGGAAGTGAACAGGAA TCGATCTTTGCTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTGGC

siSG1019 3	136 GA ---	---	---	GGACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAACCTTTAC T(G/A)TTTGAAAACTGAGATTTAAGTTGCAAACT
siSG1020 2c	143 GT ---	---	---	AAGCTAACTTAGGTGAATGGTGCCTCAAGGCTTTCCGAGGGAAGCTCAGTCCTGGCTTGGGAG AGTCAGCCTTGGTCACTCATACACGGGCTCCAAAGCTAAGGCTCAAGGAAGAGTCCCACTGCTTCT CGCTGTCA(G/T)CAAGACCACAAGGAGATGCCACTGCTGCTCTTTCCTTGTCTACTTCT
siSG1020 9b	75 AG ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAATTCCTCTTAAGATCCCACCTTAT TTTTA(G/CTCCCAATAAATGTAATTATCAGCTGCTGAAT
siSG1020 9a	34 CT ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/TAATAAACTAATTCCTCTTAAGATCCCACCT TTAATTTTAACTCCATAAATGTAATTATCAGCTGCTGAAT
siSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA(T/C)GTGAATATTTAAAGAAGTTATATTGTTTGACAT AATATGCATTGTACCCGGGCATATAAAGTTAAAGCCAGTTATCTGA
siSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAAAATCATTAAATGAAAAATGAGAAGAAATTCCTTTATTTTGGACCAATTT AGGCACCTTAAGAGTTTCTTTCTCTCCCTTCCCTTGATCA(G/C)AGTGAAGATATGATAGGGAATTC AGAAATTCCTCTCTG
EST10915 0	123 AC ---	---	---	CTGTATTAAITTAAGAAGGCACCTATTAAATGAGGACGGAATAATCTACCTGTACACAAAATCTGTAC TTTAAACAGCATCTTCAAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG(C/A)ATTTAA GAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	---	TTTTTGTAAACCAACCCCTGAAAGTTTCCACATGTGAATATAGATACAAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTTGGTTACCTATGTACAGTATCCTATACACAGTAAACAGCAGGGC AATTAGTCAATTAATAAAATAGTACATGTTA(T/A)GTGTAAATAAAATTTAAATTTACAAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGAGGGAGTAATCCIGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACTCACAATATATACCATCAGACATTGAAAACTAAGGCCATTCT GTGA(G/C)TTATTTTAAACCTTGGTGTTTGCACATAATGATCTTAAAAAAAATGAATACCAAA ACCAAGATTCTCTTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---	---	---	TGCAAAITGTGAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGTGG CAGGGATGCTTAAAGTCTTCTCTGGCAGAGACCCCGAGGTGCAGAGATGATTCCTCA(C/A)CCCTTC TCTCAGGGTCGTGGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAAGGCACCTGCCCCGCCAGACCCCTTCTAACITCTGCACACTGGAAGGT(G/A)AAA CCTGGGAGAGAGAACACACTCCCTCCTCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGGCTCAGAG

EST22917 6	74 C T ---				GTAAACCTTGAACGCCATGCTAAATGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/C/TTGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---				CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCTCAGGCTGTCTACTCA/A GTTGGTTTGTAGCCTCACTCGCACACAGGAAGCTTGAATTTGGAGGCTCCAAGTCACTCTCCA GAGGGGAACITCAAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGGCAAAAGTC/A/GTATGG GGCCAGACTGAGGTTGGACCACACAGCACTCCAAGCTGGGCCAATCCAAACCGCTGGTGAAGCGCG ACAGCAGGAGTAGCCAT
EST36745 3	56 A G ---				TGTGACCATACCAAAACCTATGCAATAAAAGAAAGAAAAAATCCTCACTTAAAAAAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAACATTCTGGTATG T/A/TJTTTGTGAGTGGTCTCTAGTGGCCAA
STS- R37410c	201 A T ---				TGTGACCATACCAAAACCTATGCAATAAAAGAAAGAAAAAATCCTCACTTAAAAAAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGGA ATTTAT[G/T]TGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAA
STS- R37410b	139 G T ---				TGTGACCATACCAAAACCTATGCAATAAAAGAAAGAAAAAATCCTCACTTAAAAAAACAAAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAA
STS- R37410a	48 C T ---				TATCGTGGGAAGTCCAACTCATACTTATGCTGCTTTTCTACTTGTAAATTTGGATGCTCTTGCCA GGCTC/C/TJTTAAATTGTGTAACTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA
STS- R42778	74 C T ---				CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGATGGTGAATAATGTTCCGGACCTAGATA/C/GTGAACGA AGGTAGCAGCAGACTGTGAGTGCACTAA
UTR- 04350	125 C G ---				GAAATAAACTAAAACTGCAAGCAAAATCACTGTTAATAAGAAATTGTTCTTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGAGCCAAATGAGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
siSG1026 6	55 T C ---				GTATAATTGAGCATAAGCCAAAGCCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT/GJAAGCAGAGTAGTACAATAATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
siSG1028 2	70 T G ---				CACCTTAGATATGAGGAAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGTATGCAAAATACAGCAAAATATTTTTCACCT/C/AJTTG TCAATGCCAATGCATTGAAAGGCCAGAAAATGAGAAAAGGATAACAAACCTTTTGTATAAAAAGGTA AGAATTCGTGTG
siSG1031 0	128 C/A ---				

siSG1847 b	95 GA ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACACAAATGCTACCCCTAAAAATGAAGAATTT AGAGGTTAAATAAACAAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATAACTTGATCACTGTGCT TCAACACAACACTG
siSG1847 a	49 CA ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAAATGAAGA ATTTAGAGGTTAAATAAACAAAGTGAGAGACCCTTACTTACATCAGTTCCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATAACTTGATCACTGTGC TTCAACACAACACTG
siSG1897 a	83 AG ---			CTTAATGCCCCCTTCTCTCTCTGACAGGAGACACAGATGGGTAAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[A/G]GCCACCACCTTCTCTCCCGGTCTCCCAAGATGACT
siSG2022 a	86 TC ---			TGCTTGAGGTTTCAATCTGAGATATCTATGGCAAGTTTATAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATATACAT[C/A]TTCCTAATCTCATCTATTTAACATTAAACACAGGCCTTTGTTGT TGTTATTTTTCTCCCTACAATATTTCTGACTCTGTAGGGACAGTGGCCTCAGTTGGGGGTTGAC T
siSG2076	104 CG ---			AAACGTTGTCCCAAAATTTGTGTTCAAGTTTCAAAAGTATAAAATAGACTTCTGAAAAAAAGTTTACA ATTAGTTATAAACAACTTAAGAATATATTTTGACATT[C/G]ACATCACAGTGGGGCATTTT
siSG2108 c	71 AG ---			TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAAAATGATTGAGGGGCTCCACAGAGA GAGC[W/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAACTAAAGCAAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
siSG2108 a	49 TC ---			TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAAAATGATT[C/G]GAGGGGCTCCACAG AGAGAGCATAAAGGGGAAGACTTTTATAGGACAACCTGTAGAACTAAAGCAAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
siSG2141 b	173 AG ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCACCTGGCATGGCGATGGTGCAGGGTGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATCTTGTTGCTCTG
siSG2141 a	113 CT ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCACCTGG[C/TA]TGGCGATGGTGCAGGTG GGTGCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGAAAGTCCCTATTATTATTAAAGGC AGTTTTCAGAGCACTGGCATCTTGTTGCTCTG

siSG2148	50 A G ---	---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACGGTGATTTC/GJAAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTTGTGATGTTCCACAGACGAGCTC ATCAC
siSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAAGCGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/T]GCCGCTGACTCAGCTAATGCTACCGGGTTGGAGCGACACCGAGCCAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGGAGTGGAAGGACCA
siSG2189	41 C T ---	---	CAAGTGGTGAAGCTGGGATTGAGCCTGATATTACACACTA/C/TCTACATTCCTCCAGTATAATA GGAATCATCGCTAACTTTGAGCACCTTAGTGTTCTGAGTACTTCGTATAGTTATCTCAATCCTACTC CAGCTTTGCGAAG
siSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGTTCTGTATGATG/T/CJTATATTTATGTAT AATGCTTACCTGATGATACCCAACATATTACTAGCCTTATAGATGAGGATGGAGCTTGGCTG GTCAAT
siSG2243	85 G T ---	---	CATTTCTGCCTCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTGTATAAATAAGTATCAA GATGGTCAGTAGAAAG/G/TAGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
siSG2257	65 A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCACTGTCTAACTCTGTGAGGAGGCTATCAGAAGGGCAG/A C/TGTCAGGAACTCTGCCAAGCACTGGGCTGCTCTCAGGCAGAAATTCCTCCT
siSG2306	67 A G ---	---	GTCATACGCTAGAGGTCACTGGTATAAACAACAAGTAGCTATATGATATTTGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATAACAACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCCTCCAGAGA
siSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAATCCCGCAAAAAACA AAAAAT/GTTCAGTGGAGGGGCTGTGGAGGGGTGAATG
siSG2339	63 T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTGCTTGACTGCAGAAGTAAGTGTGCTAC/[C] GTTCTCAGAGTCACCATACGGTGACTGTCTATTTCTGGCTGTCTTCTTATCATCA
siSG2465	76 C T ---	---	CAAGACTAAGAAGCCGACCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
siSG2549	140 T C ---	---	TTGCAGGCTGTATTCCACAAATAACAAGTCATGTATAGAGAAATGTGAAATGATACTTGAAACCAA GATATATAAAATATTGAAGTCAATTTATGCCCTTTTGTGACTGGTTAAATATGCAAGCAGCTAAAG GAATA/T/C/TACACCCACCCACCCCTTTTAACT
siSG2577	123 T G ---	---	AATTGCCAAATGGAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTGCTATCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA/T/GJGAACAATC CCGGCCAGATTAAATTAT
b			

siSG2577 a	121	CT	---			AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTGCGATTCGCCAGTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAAGCTGTGAAG[C/T]ATGAACAATC CGGCCAGATTAATTAAT
siSG2700	58	GA	---			ATCTCTCGACTGCTTAGTGGGAAAGGAATCAATTAATTAATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGGGAAATAAACCACTGGTCCAGAGCAGAGGAAGGCTACTTGAGCCGGACACCA
siSG2724 b	101	TG	---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTGCTTTTATTAATTAATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCAATCAAT[G/T]TTTTTAATCCTGGGGTGTGAAGAAG
siSG2776 a	65	GA	---			GTGGCCGATCTTTACTTTCCAGAAAAGCGGTAATAATAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCACAAAA ATATCCACTAATCCCGAATATAGTAACCTGTCGTGCCGAATG
siSG2791 b	109	GT	---			AAGGAAAGGTGGAGGGAAGGGAAGAAATTAACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAACCTAGCAATTTTAATAATATTT[G/T]GGGCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2791 a	100	AG	---			AAGGAAAGGTGGAGGGAAGGGAAGAAATTAACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATCTTCTGAACGGTAACCTAGCAATTTTAAGTAAATTTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2826	85	CT	---			CCGCAATTTCAACACACATCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAA[C/T]GAACAAAAATAAGAAAGAAAACCCATGAATGCCCAGGTTTA ATTTTTTTC
siSG2850	88	GA	---			ATGGGTGCATTGTAAGGCAATTAATACATTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCTCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
siSG3031	71	TC	---			ATACTACGGGGGCTGAAGGCAATGTGAAGAGTGACTGCAAGTCCTGGCATTTTCTGTGGTGTGAGC AAAT[C/G]CCCCCTTTATTTAATGATTCCAGACATCTGGGCAGCATAGCT
siSG3058	81	GA	---			GTCCCAACTCCTCTCCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAAGTGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAGCATCAAGCCAAAAAGGCAAAACTGGCTGAGGC
siSG3092	94	TG	---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATTCCTGTCACTATTGAAAAACAAGCCCAAGTTC CAATCCAAAAATAATAATGAACGTGCT[G/G]GATAAACATTCCTCTATGTTCCAGCCCCCTACTTT AGTT
siSG3230	95	AG	---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGT[G/G]GTGGGGTGTAAAGTGTCTGAAGTGAAGTAG
siSG3245	160	GC	---			ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGT[G/C]GTGACTTGGCTTAAGTACTTCAIGCTTTAT

siSG3265	42	T C	---				AGGTGAATGAGTTACTAAATGTAGCATTTATTATAAGGAATTC/GCATTGGAATAGTTTCTCAG TTTTATTATGGAAGATGATGATTTCAGCCACATTCAGTGATGTTTCTTAATAACACAAATCGAC AGGACTGTCTGTTCAGTACAATGGAGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTACAGTGAATTTCTGGGCTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141	C T	---				TGTACTTACTGTGTCATCCTATCCATCCCTCCCTGAGCCTGGACTGCTTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]GTAGATCCCAAGTCCCTGACACATTTTCTTAAGAACT
siSG3269 a	24	A G	---				TGTACTTACTGTGTCATCCTATCC[C/G]TCCCTTCCCTGAGCCTGGACTGCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTAAGAACT
siSG3284	130	C T	---				TTAACTCAAGAACTTTCAGTTACAGGAAGATTATCTAAATTATAAATGACTAAATACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTTAATTGCTGTAAATGGGACATTTGTTGTTGATCACC
siSG3292	99	A T	---				GTCCTAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAATAGCATTTTCTAACTTCAA TAAATGTCATATCTTAGCTCTCACT[C/A]CCAGTGATCCATTTTCCCGAGCGGTAGAGCTTTTCTG TTTCTGATGATTTGCCTGCTCGGACATTTGATATAATGAGTGCTGTATCATGTTGACATCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCTGCTCATCTTCTTTTAA
siSG3323	26	C A	---				GATCCCCAGTATTATTTCTAAATGAACTTGTGTTGGAATAAAAATCTGAGGACCACCTCAGAG GG[C/T]ATAAGGGAAACCTCTTTGTCTTAGTTTCAAGGACTTTCT
siSG3369	69	C T	---				CAAGACTGTAAAGACGTAGGCCCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAAGGAATGACATTTCCAACTGTCACTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAATAGAGACT
siSG3398	125	G T	---				TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGTGCTGGCCTGCAGGACAAGTCACCATGCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43	A G	---				GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGGCTTGAACCTCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCAAAGTTGCTGATATACAGGTGTGAGCCACTGCCCGCGGACTTTTAAACTGAAT GTTGAAAATCATCTGCTCTTGTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCCAC TTTCCCTTATCTGTAAACAAATGGACAACAGAACTTTTCCCTTTCCTCTC
siSG3424	173	T A	---				GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGATGGAGGCTTCACAGA ATGAGTGGCAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTTCCTATC
siSG3436	88	T A	---				

siSG3463	103	C T	---			GATACAGAAGATAGTGGTATGGATAGTATGAAGGACAAATAATACAAATATATTTATG AAATAAACAAAAATGCATACACAGCTCAATGGGTCA[C/T]TGGAAACAACTTGCTTGACTATATTA CTGA
siSG3491	71	G A	---			CAAGATACCTTCACTCTAAGTAGTGCAGTGGCAATAATTTCTCAGCAACAGGACGATTG AAGA[G/A]GTGGAATTAAGTGAAGGAGTACTTTACCTCCAAATAGCTGCAATTTAGCAGTCTGA ACAACTTCTAATCTTTACTGGCACCTGTGGATTCTTATAAAGTCAATTTACTATTTCTGTGATG ACAGAAAAATAAGTTAAG
siSG3523	33	C T	---			TAGCCATCTTACTCTAGTCTTTTGGGTTT[A/C]TGCAATATATGTGTACAAACACACACACACC CCTAATCTCTCAAAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
siSG3536	213	A G	---			AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGTACAAACCCAAATACAGAAATGGCTTC TGTGATACTGGCCTTGTGAAACGCACTCTCAGTCACTTATTTGTTTATTTGTTAAATGAGCTTG TGCACCATTAG[A/G]TCCCTGCTGGGTGTTCTCAGTCCCTTGCCATGAAGTATG
siSG3583	112	G A	---			GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAG
siSG3586	60	G C	---			CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATTCAGGTGGTGGT[G/C]ACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
siSG3589	101	T C	---			ATATAGTGGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCAACCCCTGGCACAACCAACCCCAATGAT[C/C]CTATTTCCAAGAATGTATCCAGATGAAA GTATCCAACAAACAAAGCTATATACAC
siSG3590	70	A T	---			GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGAAGAAATGATCTTCTGTTCTAAAAAAA AAA[A/T]TTTCTCTGATGCTCTTGTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
siSG3619	78	A C	---			CAGTGAGACTTCTCAATTTATAGCAAAATACATTTTGGAGCTTAAATTTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAACTCCAGAGAAAACCTGGGCTCTATATATTTAAG
siSG3644	40	T C	---			ACATATGTAAGTGGCATTAGTAGCCATATTAGGATGAGAT[C/G]GATTGAGAGGATGAACCAAGG ATGCGTAATAATCATTATGAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
siSG3646	70	G A	---			CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATGATGATAACAAATAATATGCTTACT GGT[G/A]ATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

siSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATGATGATAACAATA[A/G]TATGTCTT ACTGGTGATTAATTAACCTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATTAATTAACCTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TGGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAGG
siSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]CTGAAAGCCGATGACCATCCAACCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAGG
siSG3698 b	145 G A ---	---	TCTTGCCCTTTGTTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCGAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
siSG3698 a	51 C G ---	---	TCTTGCCCTTTGTTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
siSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCACTGGAGCCATCCCTGGGCCTAGACTTCT GTCTCCCTCACCTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
siSG3725	104 G A ---	---	GCCAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAATATATTATTACAGCCAAACAGCAACAGACGCC[C/G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
siSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCTATACCTTTTAGAAGATGATTTTG AGGGCTTCAGTATTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
siSG3787	49 T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT[A/JAAAGTTCCCTAAGA CACTGAGGGCATAAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
siSG3880 b	115 G C ---	---	GACAAGGGAAGAGATGCGCCAGAGACCAAGGGCTGGGGAGCTGGGGGTCCCTGAGTCCAGGGCG CACCACAGTCTGTGGTCAAGGCCCTCTCTCTGGGGAGCAGGTCTA[G/C]GGCACGGAGGATGCAG GGCTGGGAGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT

siSG3880 a	36	G C	---			GACAAGAGGGAAGAGATGGCCAGAGACACAGGGCTG/CJGGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACAGTCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGCTAGGGCAGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT
siSG3895	44	A G	---			AATCAGCCATTGTACACATTGCAGCTATGTATTGTTGTTG/CJGTTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATTCOAATTAGTTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
siSG3902	104	T C	---			TCTGTTGAGACTGGAGACAGGTACCAAGCACGACTCTGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACTAAATGTGAACCTGCTTTCTTTCT/CJTCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
siSG3935	50	G A	---			GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCCG/CJCTAGTGTCAGGC TCCTCCCGAGTTTCCACAGGCTGAGTACTATGGGTCAACAACCTTCCTGGACGT
siSG40	25	A G	---			GAGGAAGAGGTTGAAGAAGTGTG/CJGAAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAATAAACCCCTTGTTATGTATCA CCCA
siSG4009	32	A G	---			GTGTGGGCTGTCTGATGATGAATGGCGGCTC/CJGTACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGGCTTTAAGGGCTGAACCAATCTGAAGGTTTCCCACACTGCTTACA
siSG4033	123	T C	---			AGAAGCCTTGGGACAATGGCAGTGCCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTTT/CJGTGAAC AGGTGGGCAACAC
siSG4038 a	29	G A	---			GCTGAGAGCACGTGTACAGCCACGCCTG/CJGCGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
siSG406	53	T C	---			ACTGTGTTCAACAGTATTGCGTTGTACAGCTAGGAAAGCTAAACGAACAAAT/CJGGTTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTCTCAACAAGAGATTATTAACTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T	---			ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGTAGATGTATTAG/CJTATAAAAA GTTTGCTTCTGTAATAGCTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCCCTGG
siSG4095 a	27	A C	---			ATCTGGGCTGAATTAGTCAAGCAGGTC/CJGATACTATTGTCTGTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATAGCTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCCCTGG
siSG4120	65	G A	---			TGCATGTTCCACATCTTTTCAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC/G/ A/CITTTTCCCTCAGAGAGGCCACAGTTAAACACGTTCCAGCACACCACTTAATCCACCGAGCT

siSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTGTTTGCAGATATGACTTTCCTTTGGTACATTTCTTGGTATATTTT TACTTCTTGAAAATGCCACATAATTTGCAATAATGATTCACTCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
siSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGACAGAGCGGCACTCCCTG/GA/GC AGGGGACCACGGAGCGACAGGTCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACA/G /A/CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGACAGAGCGGCACTCCCTCGGC AGGGGACCACGGAGCGACAGGTCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACACAGAGC/GA/CACGGCCGGGACTCCCGCGATGGCTGGGGG GCTATGGCTCTGACAAAGAGGTGAGCGAGGGCCGGGGCTGCTCTCCCCCAGGGCGACGCTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCA/G
siSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAAAATAAA/T/G/AGCTTCTGAGTAGTGTTCOCAGTTTCAACCAACATTTTG
siSG4331 b	71 T G ---	---	CTCACAAGGGCCACACAGAAAAGATACAAATACATTCACAGCTAATATTTAGTTTATGACAG AGAGT/G/TTTCAAAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCCTCGCCTTGTGATCTGTTTGAGGGGTGTGC
siSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC/GA/TAAGTGGAGATAAACAAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGCG/C/C/CTTCACAACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4361 a	24 T C ---	---	TTCCCAACCATTTGAGTGACAGAGC/T/C/AGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTTCTTGAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4376	73 A G ---	---	TTTCACTGCTACTGTTTCGGTGTCTGAGTCCCTCAAACTCTGCTTTGCAAGTGTCTTCCAAAGGGGAG AACAG/A/G/CTGGAATGCGGCTCTGCAAGAAAGCCATCTTTCCAAAGCCATTTCTTCTCAGCTGC
siSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTTT/C/TCAGTCTTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAGTGTCTGTCCAGAACCCCATTAATTTCCATGCC
siSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTGCATCCGATAATTTTGCCCGATCTGAAATCTGCAAGGGCTTAACCAT TCAAAACACCGG/C/G/ITGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

siSG443	65	C T	---			AGCAGATCAGTCAGCCCACTTGCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
siSG4430	54	A G	---			TGTATGCAATGAGAAATACCAACTGTAGGATGGGGAGGGGAGGGAGGCAGGGAATAGGCAC
a						AAATGGAATCTATCTGCTGCTCTCTCTCAGGTC
siSG4448	99	G A	---			ATGCACATTAAATGAATGGCCTACTACTGGAACTTTAGTAGTCTATAAGGTJAGJATTAAACATA
						GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
						CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCTCCGCCCCACCCAGGCTCT
						CGCTAGCCCTGCCCTCTGGGTCACTGCGJGJATGGGTAGGCCCCCAAAAA
siSG4449	92	T C	---			ATTAGCAATTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACTTTGGACAACCTTAAACTTA/TJTAGTGACATTGCTGCTAATAATCAATACTTTCATCATA
						GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
						CAGACATGAGGGATGGCCCTGCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
siSG4467	42	C A	---			GAATGAACTCAAACTCTTCACTTTTAGAGTCAATTTCTGGTATCGAGCGCACACACCGAGGAG
						CACACCCTGCTTCCAAAGGCTGCTGCCCTCTGACACAGT
siSG4475	21	A C	---			ACATGTCATTTCCTGACCAGGJACJATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAACCTGGACTTTGTTTCTTTACTGTAGCACCCAGGTTTCATG
						GTAACATCTGGGGTGGGGTGAGACAACA/CJATGAACCAATAATTAAATTAACATTAACATT
						TCAAGGAGACTTTAATCTAGTTAATGTGAACGCAACCATCAATGGTTGTGAGGAAAAGGGAGA
siSG4477	32	A G	---			TGAAGTCTGCTCTGGGGCAACGTTTGGCTCATTCAGTCAGACTTGGC
						TGAATCAGAGCTGGTGGGAGCTGCAGGCGAGGGAGGCTGGGGCCCGCAGATGAGCCGCCGGGA
siSG4531	79	C T	---			CAGCAGGCGTGGJCTGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGGCTTGGACTCGATCT
siSG4550	86	G A	---			GATTCATTGACAGGGGAGACGCTGTGTCATCAA
b						TGCATTAAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
						AAAAGAGACAGTGGGCACGJGJCAATTGGAGGGGAAGGGCGGCGAGGGTTTATAGAGAAC
siSG4550	85	C G	---			TGCATTAAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a						AAAAGAGACAGTGGGCACJGJGCAATTGGAGGGGAAGGGCGGCGAGGGTTTATAGAGAAC
						AATCAGGCACAAGCTCGGAGAGAGCCAAACAAAGCTCTCTGCACJAGJATGGGAGGGAGACAC
siSG4590	47	A G	---			CATTGAAAAGGCATCGTTCTTTCATGCAAGCGAGGCTGCCACAGGCGATGGTCTCCTTG
						AATCTGTATCACCCAGCGTGGT/CJCAATGTACTAGTACTTCCACAGGGATTTTTTACTATTTC
						CTATAAGGTTTTATCATGAATAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCATTTATCT
siSG4623	22	T C	---			TAATATCTGTTCAGATGCTCTGGAG
						TAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTGTAGTTTTATGTTTTTTCAGATTTAAAG
						GTAATTTCTTTCTTAGCTTCTAAATTTTGTAGTCATJACATCAGAAAGTCTTCCCTACTCCAAAGGTGA
siSG4843	102	A C	---			GAAAGGA

stSG4850 a	38 C T ---	---	---	GGAACTAACTGGGAATGCCGAGGAGGAAGGGGCTC/TGTCACATTCAGGCCACGTCAGGAG AGCCAGCGGTGCTGTGGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86 A G ---	---	---	AACCTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGGTCCTGCTTTTGCAGAATGGCCTG CCCCTGGGACTGGAGCAG/GJCTTGGGTGAGCTAGGTGGAGGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---	---	---	ACTGGACTGGCTGCTTGTGAGCCGGCTGAGCGGGTGGGACTGGGCTGACCACTCGCTCTTCAG AGACTCGCCCGCGGTGACCACGACTACGCTCTGCG/GA/GTGGGAAAGCAGAAAGCAGGACC
stSG4896	112 C T ---	---	---	AAACAAATCAAAACCAATCCCAGCAGTCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTTGGGGGCAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCT/TGAGCCACAGGCCCTGAGG AATTAAATTGACTG
stSG4932	22 G A ---	---	---	ACAGTGCCGATGGTTACACAAT/GA/JTGTAAATGTATTTAATCCCACCTTACGAATGATTAATAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGGCTGTGGGTGCAAGGGTGTGTTTCTGTGCT
stSG4950	24 A G ---	---	---	TCATGACTCCCAGGAAAGGTCCT/GJCTTGTAGCTTCCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCAITGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	---	AGATACGGCAAAACACTGGGATGGCTTCTGACAACCTTAAGAGGTCCTCCGAGTTATATTCTGGGTT GGGAACACTGACCCAGCCCTTATTCCTTCAAGGACTAGTCATTGGCAAGGAGGATTCATGAGCC CC/GA/GTGACACAGATGGGGCCCTGCTCTATATCAAC
stSG4961	91 C T ---	---	---	GAAGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	---	ACTGGTGCTCTCAGCAGATTCAGGGGTGTCGAGGGGTGTTACCACAACTCAGTAGGAGTGCAA GGGCT/GJTAACCCCGGAGCTAGACAGCCCTGGGTTTGAATCTCAACTCTCCCTTTTCTTGCTGTGC AACCTTG
stSG4997	22 T C ---	---	---	CAAAGGAGAGTAGGAGCCCAA/T/CJTTTTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T ---	---	---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/C/TJATGTCATGCGGGAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---	---	---	GCTCTGGTCAAGCAAATCTCCAGGACAGAGCAACAAAGGACAGTAAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC/GA/JATAGTTGAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAAACATTTTGTCTTTGGCCTGGGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGCATG

siSG6362	88 G C ---	---	TGTGAATGTACACTCAGGCTAACAAATACCTATTATTCTCTGTTAAGAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
siSG8010	62 G T ---	---	CACATCTGTGTTCTGGAGCAAGGGAACACAGAGCCAGGAGTTGGGTGTGCACTGG[G/T] GTCTTCAACTGGGTGGAACCAACTGAGTCCTTGAAGTCGCTCCTGAGGCTGCAGAGAATAGA TGGCTT
siSG8022	53 G A ---	---	AGTCTCTGACTCCTGTTTCAGTGACGTCATGTTGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAACTGGAAACTCTACAAATCAATGCGTTATTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC
siSG8032	67 G C ---	---	TGATTGTTAGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAGAATTCAGAAAAATTGTGTGTT G/C]TGGGAGGAGGAGTACAGATAAAAGAGGAGGAGCAGCTGGGTTGGTAAAA
siSG8064 b	46 C A ---	---	AGCTGGCTCTTCTCTGTGCGTGTTCGGGAGGCTTACGTCCTCG[C/A]CGGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAAATCCTGTACATCAACACAGGGAACA
siSG8064 a	23 G C ---	---	AGCTGGCTCTTCTCTGTGCGTGTTCGGGAGGCTTACGTCCTCGCCCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAAATCCTGTACATCAACACAGGGAACA
siSG8072	59 A G ---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGCTTCTGTCTTAGGG[G/G]TGGC AGAGGAGAAGGAAGTCCGAGTATTAGTGGCCGATCGAGTCAAGCCTGTGCTGTTCAAAA
siSG8100	40 A G ---	---	ATACACCCACACACCCACTCAACCTTGTATCAAAATCC[A/G]AAGTGAACATAAGTATAAGAAT ATCATGACTAGTTAAAGATAGCAAAATACCAATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
siSG8102	138 T C ---	---	AAGGCTCCTTTGAAAGCATGGTTATTGTTCCATTAACTGTTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGATACAAATGTGAAA TGAT/C]GTGCATAATCAATAATCAATAATTGGTATATTGGTTAGGAATGTGATGGT
siSG8105	110 A G ---	---	CAGTGGTTCCTCAAACTCCAGCGTACACGAGGATGGTCTTGCTTGTAAATACACAGATGACTAGGCC CACCTGGGAGTTCCTGTGGAGTCTAGGCCCTGAGAAATTC[A/G]TTTCTAACAAAGTCCCAGGTGA CCCTGAGGCTCTTGACTGGGGAACATGCTTTGAG
siSG8130 b	96 T C ---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTGGCTGCTTTTAAGTTTCAAAAT GACATTCCAGACAAGCGGTGCTGAGCCT/C]GTGCTGTCTTCAGATCTTCACAGCACAGTTCC
siSG8130 a	36 C G ---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGA[C/G]TGGATGTCGCTGCTTTTAAGTTTCA AATTGACATTTCCAGACAAGCGGTGCTGAGCCTGTGCTTTCAGATCTTCACAGCACAGTTCC
siSG8145 b	124 T A ---	---	TTGGGAGCTTCAAAATTCCTTCTTCAGATTTTAAATGACATTATGATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATGTGAACACAAATCTAAGAAATGAATGAGATGTT[A/C]TGAAA TCTGATTCAAAAGACTTATCTTAAAGTGAATGCTGTCAATCTCTGTCTGTGAAGG

siSG8145 a	97	C T	---	---	TTGTGGACITTCAAATCTTCCITTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATGTGAACCTGACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAACACTTATCTTAACTGACTCTGTCATCTCTGCTGTGAAGG
siSG8150	36	A G	---	---	ATTGTTCTTGCAATTGCTGGATTTTTCAGAATAGTJAGJATAAATAAACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTCTGCTATTAAATACCATGCAGGAAAT GGGAAAT
siSG8340	30	C T	---	---	AGAGGATTATGGAGAGAGCTGGGAGGATCTTCAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAAGAGAGAGAAAAAGCTCATCAAAA
siSG8466	111	G A	---	---	TGTGATTGGGTGACTGTAGCCTAAGGATAAATAATGAAATAATGACAGCAATGTTTAAAGCAGTGGGA GGAGTGAAGTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCAATTAT TTGAAAG
ESTD-ACE	--	--	---	---	GATCAAGGAGTGCACAGGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAGGATCTGCCGCTCTCCCTGCGTGGGGGCCAACCCCGGCTTCCATGA GGCCATTGGGACGTCTGGCGCTCTGGGCTCCACTCTGACATCTGCACAAAATCGGCCCTGC
ESTD-ADA	--	--	---	---	ACCATCTTATCTATGGCAGGTAGTCCATACAGAGGCCCTCTCTCCCTGGGATTTGAGTGGGTC CCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGCTACTTCTCTCTGCTGCTGCTGCTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGCCCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTTGGGCCCTCTGAGTCTGTGCTC
ESTD-AK- 168	--	--	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	---	AATCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACAGAGGTGAGGATTTGAGACCAGTCTGA CCAACATGGTGAAACCCCATCTCTACTAAATAACAAAATTAGCCAGGCATGGTGTGCATGCCGTG AATCCAGGAGGCTGAGCAGGAGAAATCGCTTGAACCTGGGAGGCGAAGGTTGTGTGAGCCGAGAT GGCACCATTCACCTCAGCCTGGGCAACAAGAGTAAACTCTGCTTC
ESTD- ANT1	--	--	---	---	TCTCCTGTCAATTCCTACTCCATTAGTTCAAGGTGAGTGAAGAACTGGGGCAATTAAACCAAGTAATCA TGGAGTGCCCAACTCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGGCGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD- APOA2	--	--	---	---	CCAGGTGTTGTGGCAGTGCCTGTAAATCCAGCTACTCGGGGAGACTGAGGCATGAGAAATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGGCCCACTGCACTCCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD- AFSB	--	--	---	---	GGAAGAAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGGTGGCTTTGTGGCAAGGCCCTTGTCTGA AGCAGAAGGGGTGAAGAACCGGAGCTCATCCATCTCTGACTGGCTGGCCAACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTGGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATGAGCTGCTGCATAATATTGACCCCAAC

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTTGTAAAAGGGAAGTTGTTCTTGATCTCCATGGGCCAGCCAGCACTG GTCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCCAGGTGGAGAGAAATTTGAAAGGGCAATTG GAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGAAATGTGG
ESTD- B3AR	--	--	--	---	---	GGCTCCAGGGGTTCTGTGGGAGGCGCCCTAGCCGGGGCCCTCTCTGGGCTGGGGTCTGGCCACC GTGGAGGCAACCTGCTGTGTCATCGTGGCCATCGCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCGTGGCCCGCAGCCGACCTGGTGATGGGACTCTGTGTGGCCGCGCGGCCACCTTT GGCGC
ESTD- BA511	--	--	--	---	---	GGCAACATAGTGAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGCTGCAG TGAGCCAAAGATGGTGCCACTGCA
ESTD- BCL2	--	--	--	---	---	AGCTGGATTATACTCCTCTCTCTGGGGCCCGTGGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAACAGGGTACGACAAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGCAGAGGGGCTACGAGTGGGATGCGGGAGATGTGG CGCGCGCGCCCGGGGGCGCCCGCCGACCGGGCATCTCTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GACCAAGAGGTCAGCTTCTGTTGCCCGGAAAGGAGGCGAGGTGACAAAGTAACTCTGCTTCAAA ATCAACCATCGGTGGACACTGTGGCTGCCATCTGCTCTGGCACA
ESTD- BRCA1a	--	--	--	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCACACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGTACCTGTGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTTGGAAAGTTAGCACTCTAGGGAAGGCAAAACAGAA CCAAATAAT
ESTD- BRCA1b	--	--	--	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACTGAAAGAGAA ATGGGAAATGAGAACATCCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTGTAATAATGACATTAAAGGAAAGTTCTGCTGTTTTTACGAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTACCCCATACACATTGGCTAGGGTTACCGAAGAGGGGCCCAAGA AATTAGAGTCTCTCAGAAAGAACATTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTTAATTGCTCCGGGAAGCACATTCATCAA CCAGTCAAGTTGGGGACAGCCATGCAGTGAAGCTCTGTGTAGCCCTTTCAACCATTCGATTCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	

ESTD-C7	--	--	--	--	--	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCTCGTGGGA
ESTD-CB22	--	--	--	--	---	GGCAAGTTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCCAAACCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAG TAACATAATTGCTCTATTATGCTCTTCCCGGCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	TAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACCGAGGACGACAGCT CTCAGAGCAACCCCTAGCCCATTAACCTCTTCCCTTTCAGAGGACCTGAAAAACGTGTTCCACCCGA GGTGGCTGTGTTGAGCCATCAGAACGAGAGATCTCCACACACCAAAA
ESTD-CB24	--	--	--	--	---	ACCAGGACGACAGCTCTCAGAGCAACCCCTAGCCCATTAACCTTCCCTTCCAGAGGACCTGAA AAAGGTGTTCCACCCGAGGTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCCAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACCACTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGGTCAGCACAGACCCCGCAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	GTTTTCTTCAGACTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTCGCCGTG TCTGCTCTGAACAGGGCATGGAGATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTTGTCACAGAGTCTTACCGCAAGGGGTCTCTGTCTGCCAOC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	--	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGCCTGGTTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAGCAGCATTCCTTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGTCACCTTCAGGGGTTCAGGGTGGAAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCGCTTTG GTCAGCCTATTGAGCTGTAATCAACATACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAACACTGGACTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTATGGCAAGATATACAATAACAATTTTATTTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAAC TGGAGGCGCGGCATAGTGTCTGCTGATGCCGTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCCAACAT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTGGCTTGGAATTCAGGGCACAAGGCTCAGCTGAACCTGGGTACAGGACCTGGCCCTGCAC TCTCTGTTTTTCTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCGGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCCAGGTGGTGGAGGTGGTCAACATCCCGGCAGAGAACAGGTGACGCCACCACTATGCACAGGT TCTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAACAATTTAACACCTTTTCAATCATATACACCATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAATTACTTGCAATCTAAATGTCATAACTGATTAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCATCCTTAGCACCTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCTCTGGGGCGGTG GGGTGTGGCTATGTGGTGTCTTGTGTAGACGGGGCTTTGGTTTTCAGTTGCACATTTGCGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCAAACATGGCGAATCACATCTCTACCAAAATTAACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGCACTGAGCCAAAGATCACACCACTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACGTATTAGAACCCTGAAAATACATATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTTGT TTATTCAACTATTTATCACCTATTTTATTGGTAAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTAAATCAAGGTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTTCCC AGAAGTGAACACATACTGCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCAAGATGG CAGGTATGAATATAATAATCTGTCTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTCTGTTTACCTGTTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATGAAATGTATTT CTTAACAATAAATCTGAAAGTCCAAAATTTACCTTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTTGGGTGACCCAGGTGTTT GCCAATAAGCAGTAATAATTTTGGAGGGAATCTTGTTTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTTCATGCAGATAGGCTTTCTCTACTAATACAGAAATTTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGCAATCACTTTCTTTCTTTCTTTTCTTTAGAGTCTACCCG

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ESTD- D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTACAAAATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAAACATGACAAAACATTTTC
ESTD-DM	--	--	--	---	---	GTGGGGACACGAGGGCTCCAGGCTGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGTGGGAGGGGAGACA GAATGCTGATTATCTGTTGGAGAACCAAGAACTTCTGGCTGTGGCTGAGGCGAGCTGCTTCCAAAGACC TCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGACAGAT
ESTD- DRD1	--	--	--	---	---	TCCCCAGCCCTATCGGTATATTGGACTATGACACTGACCTGCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGCTGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	TCTGCCCTTGGTCAGGAGGCTGCCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCACCCAGCTGACTCTCCCGACCCCG TCCCACACGGTCTCCAGACACTCCCGACAGCCCGCCCAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG CACTGTGGAGTTCTGCCCCACAGGTGTAGTTAGTTAGCTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB82	--	--	--	---	---	TCTTTACAGGATCCGATCTGGCCTGTGTTGGCATCGCTCCGCTAGGTGTACGGCTCCACCCAGCTGG GGTGAGGGGGTGGTGGTGAGTGCCGGGGGCGGGTGCGAGACCCACCGGGCTGGGAGGACTTCAACC CGCCTCACCTCCGTTTCTGTCAGCAGTCTCCGCTCGTACT
ESTD- ETS2	--	--	--	---	---	ACTCACAGTGCCTTTAAGTGAATGGTCGAGAAAGAGGACCCAGGAGCCGCTCGCGCCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGCTGGGACACACAC AGACTATTTTAGATTTCTTTGCCCTTTTGCAACAGGACAGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAAACAACCATGTCATTTTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACAAATGGCTCCAAAGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCGGCCGGTGGCTGGTCCCAACAGAGGAGGCGCTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATTTGTGTAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- GCH	--	--	---	---	---	CGCAGACCGGTGAGTGGGGTCGGAGTGTGGAGGAAGGAGGAGGAACCTGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTGCTTGCAGAGAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGACCTCTGGTGCACCGTGTCTGCTGCCCTGTTACGCTGTCTGTCTGCGCGAGTCGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	---	---	---	GTGTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCCCACCCACACCTGGCTGG AGCAGGAATGCCGAGCGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCCGAGGTACAG
ESTD- GNAT2	--	--	---	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD- GPPK2L	--	--	---	---	---	AGTCTCATCTGGGGTGTCCAGGTAGATCCCTTTACCGCCGCGAACTGCTCGATATC
ESTD- HRAS	--	--	---	---	---	CTGGCTGCGCCGAGCAGCTGCTGGCACTGGACGGCGCGCCAGGCTCACTCTATAGTGGGTGG TATTGTCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	---	---	---	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCACATTTCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAAAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTGCGCCTCCGGCTTGATTCC AGATGGAGCTTCCCTTATCCCTGATGATTTGGATTGGCTTCTCTGCTG
ESTD-HT2	--	--	---	---	---	GGGCTAAATTTCCGAGCAACTTTCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTACAGAGAATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAGACACACCTT
ESTD-HT4	--	--	---	---	---	ACCAACGAGCGCGATACAGACACTCTTAAGTTTTCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTGGGTGCTTCTATCGGCAAGATGCGTACTATTTGAATAGTAGAGGTAA ACCACAGCCCCCAAGAGTCACTGAGACTGGCAGCTTCTGACGAGCGGTGAACCCCGTAGCCCTAAA TGACAGCGGAAGAGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	---	---	---	AACACACAAGCCCCAGCGAGAAATTGAACCTCGCGACCCCTGGTTTACAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTCTCTCTTCACTCTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTACAAAATGAAA ACATTTCTGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	---	---	---	ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGGTGCCCTGGGAGAGAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	---	---	---	TTTACTATTTCATGGATACAGAAATTGTGGGAGTCACATATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTCCCTACATTTGTGTAGTGACGGGCGAGTGGTGAGTCGGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGAGTAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	---	---	---	CAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTTATTATTATTATTATTATTTTGTG AGATGGAGTCTGGCTCTGTCAACCAGGCTGGAGTGGAGTGGCAATATCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCCTCGCTCAGCTCCGAGTAGCTCCGGAATACAGGCACCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTGGGTGCTGTTCTCTGCTCAGGAGCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCATTTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTCTAAG AGAACTGTACATGACAAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACAGATTGATA
ESTD- KRT8	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGAGGGCCTGAGATGAGCCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATAATTTCAAAATTTAAACGTAGCAAACTGCATTGGTATTAGA AAAAATAAAATTTCCAATATGTAGTGTGTTTATACCTGCTCTGCCATGCAGCATCATAGCCTGT GGGAACCCAGGAGGCTCCCTTACCACCCAGA
ESTD- LMP2	--	--	---	---	---	TACACACTTCTTACCCATTCACTGAAAGGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	---	---	---	TGTCAGTGTCCCTAGGGCACCTCACCACTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGGTTTGTGTTAATCTCAATTCAATGTCTCTTCACTTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTAGTTTTTAATTATAAAGAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATAAAATTTTTTCACCTG
ESTD-MCC	--	--	---	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGCCCTAGCGAACTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAAGGGTTTTGGTCTAAGTGTGCTAATACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	--	--	---	---	---	ATTATCCAGATGAATTTACAAAATACTATACCAGATCCACAGACTGATGCTGGT

ESTD-NFKB1	--	--	--	---	---	AAACATGGACTTGTATATTGTACAAAAAAGTTTTTCTAAAAAGAAAAAGAAAAA
ESTD-NPBA	--	--	--	---	---	AAATTTAAAGGGGTACTATATCCACACTGCACACTGCCTAGCCCAAAACGCTCTATTGTGGTAGG
ESTD-NRAMP	--	--	--	---	---	ATCAGCCCTCATTTTGTGCTTTGTGAACCTTTGTAGGGAGAGAAAGATCATTTGAAATTTCTGAG
ESTD-NRAS	--	--	--	---	---	AAAACCTCTTTTAAACCTCACCTTTGTGGGGTTTTTGGAGAAGGTTATCA
ESTD-OTC	--	--	--	---	---	TGTCCTAGGCCAGCCCTGCTTGCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC
ESTD-PAI1	--	--	--	---	---	AT
ESTD-PAR	--	--	--	---	---	GGAGCAGGAGGTGGGAGGGGGTCTGCTGCAGGTCCACAGACAGAGAAGCGGCCCTCAGTG
ESTD-PBDA	--	--	--	---	---	TATCCCCACCCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGSCAGGT
ESTD-PS-1	--	--	--	---	---	GTGTTTTCTTAATCTTTCOCAGGAACACAGTGACCATAATTTCTTCGAGGCATATAGAAATTTGGT
ESTD-PXMP1	--	--	--	---	---	GGTTTTCTTTTATAGGGTGATATTGGATACCTTTTGTGTGATTATATATTAGCAATTTGAGGG
ESTD-Per/IRDS	--	--	--	---	---	ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTAACTTGGCAATAGCATTGC
	--	--	--	---	---	ATCCCTGTGGTTTTTAATAAAAAAT
	--	--	--	---	---	GTGACCTTCTCACTTTAAAAAACCTTTACCGGAGAGAAGAAATTTAAATATATGCTATGGCTATCAGCAGA
	--	--	--	---	---	TCTGAAATTTAGGATAAACACAGAAAGGAGAGGTATGTAACA
	--	--	--	---	---	GCCACCACCCACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTACACAAAGAGAGCCC
	--	--	--	---	---	TCAGGGGCACAGAGAGTCTGGACACGTGGGAGTCAGCGTGATCATCTCGAGGCGCGCGGCAC
	--	--	--	---	---	ATGCGAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTTAGACAGACAAAAACCTAG
	--	--	--	---	---	ACAATCACGTGGCTGGCT
	--	--	--	---	---	CTCTTCAGGAACCCAGCTCTCTTACCACACGACTTATTTGCTGCTCCGAGAGGTACAAACCCGTAGA
	--	--	--	---	---	ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT
	--	--	--	---	---	AATGACTGGCTTTCATTAGCTCTGTGAGTGTTTTCTTCACTTTCTGTGTTCTAGAACGTTTTCTAG
	--	--	--	---	---	GACTGGCAGTTTAAGCTTCACTTAGGCTTCTGTATACCCATGCC
	--	--	--	---	---	CCTTCTCATGCCAGATGAAATTCOCAGTCCCTTCAGGATCTGCCTAACCTGTACAGTCTAAAGAGT
	--	--	--	---	---	CTGAGCGTGGCTGGGAAGGCGAGGACTAATCCAAATCTCTACCGCAGCTTGCTGCGCATACAGACG
	--	--	--	---	---	GACAGTGTGGTGCAACATTGAAAGCCTGCTACC
	--	--	--	---	---	GGGGAGTAAACCTTGGATTGGGAGATTTCAATTTTCTACAGTGTCTGGTGGTAAAGCCTCAGCAACA
	--	--	--	---	---	GCCAGTGGAGACTGGAACACACCACTAGCCCTATTTCTAGGCCATAATTAATGGTTTGTGCCCTACATT
	--	--	--	---	---	ATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAAATCTCCATCACCTTTGGGCTTGTTT
	--	--	--	---	---	CTACTTTGCCACAGATTCTTGTA
	--	--	--	---	---	ATGAAACATGGTCTTTAAATTTTATGATATGTTGTTATAGCTATCTTAAAGGGGCTCTTTTTTTTA
	--	--	--	---	---	ATGCAGAAAGAGGGGAAAGAGGAGGAGCTGTGGTGACAAGGTGTTTTCTCAAGGCTCATACAGA
	--	--	--	---	---	TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGCTTATGAAATTTAATCTT
	--	--	--	---	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG
	--	--	--	---	---	CTGGAGAAGAGCGTGCAGGAGACCTGGAAGGCCT

ESTD-FDS	--	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAAGAGCGTGCCGGAGACCTGGGAAGG CCTTCTGGAGAGTGTGAAGAGCTGGGCAAGGGAACAGAGTGGAAGCGAGGGCGGCGAGACGAGG CCAGGCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAAACACTGAGAAATAGTGCAC CCAAAGAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	--	---	---	CTTCGTGACGGGAGGTACGCTCCGCTCTTCATGGACATATGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGTATGACAGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCGCGC TCCCTGTGAGGCTGGAGCACTGAGAAATCAGCTGAGTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTACCCGAGG
ESTD- SPTB	--	--	--	--	---	---	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTCTCTCTGGGAGCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGCCACCTGCTGGTTGAGCTGGACATACACCTTCACCTCTTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGACACCCCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCAGCCAGTTTCTCTAGCAAGGCGCAGGAC
ESTD- SSA1	--	--	--	--	---	---	TTCACTTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCCTTGGCTGCCTGTGCTGTGGGATATTGAAGAGATCTTTGCCAGTCCCAATGTCTAGAGAG TTTCCCAATGTTTCTTGTATAGTTTCATAGTTTGAAGGCTTAGATTTAAGTCTTTAATCCATTTTG ATTGTATTCTGTGA
ESTD-TAT	--	--	--	--	---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATTCATCTTAAATGACTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTTCTCCAGTATGGATGGGATTTATGATGGGGG GAGAAGCAAATTTTAAATAGGACCCATGAGACATCA
ESTD- THRB	--	--	--	--	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	--	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCTTGTATGCTT GTGTGCCCAACTTTCCAAATCCCCGCCGCCGCGATGG
ESTD-TYR	--	--	--	--	---	---	TAGTGAAGTTTTTCATCTCCTGTGAGCTCTGAGTTCTTGTTCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGTGCTTCATGGGCAAAATCAATGTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATATGATCCAGACAAAGAGGTCAATAATTTGATGTGCGTTAAACAT GGGTGTTGATCCATTTCATTTTGGCCATAGGTCCTATGGGGATGACA

ESTD-TYRP1	--	--	--	---	---	---	AGTAGTGATGAAGCTAACAGGCTCTCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGCTAAGAAATGCCCTACTCTCTTATGGATTAGTATCAGAA AACCACCTGGTTGAATATATAGATTGAGTTATTAAGTGTATTTCTTTTCACCTTTATTACCTTCTCTTCT AATACAAGCATATGTTAGAAITTAAGTTCTAGGCATACTT
ESTD-VB12	--	--	--	---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACAA GGACACATGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACACAGTG ACTCTGAGATGTCACCCAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	--	---	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCCTCCCTTCCTCTTACTCTCTGCCTGCAGGATGTG CGACGTGTCCTGGAGTAGCCCCGACTCTTGACGGTCGSCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	--	--	--	---	---	---	TTGGGAAGTTAGAGCCTATATTAAATACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCCGTTAAC TCT
EST71770 6	--	--	--	---	---	---	AGCACACCTCTCAGTCAAGCCTCAGCACACAGATGCTGTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAAAACCCTGCAGAGTACCAGCTGTGTGGTGAAGG AGTGCCACAGTCCACAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAGG
EST52418 6	--	--	--	---	---	---	CAAATTACAGSGTCAACTGCTATGATGTGTTTGGAGCCAGTCAACCTTTGGTGGCTACAAGATGTGG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAGAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	---	CCCCTCTATTGCCAGCCCCAGGACAGAGCTGATCCTTTGAACCTCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCACGCCACAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCCCTGCCCGG GTCACTC
EST51976 7	--	--	--	---	---	---	AGGCAGAAACTGGGCCCCCATGCGGGGGACGTGGAAGGCACCTTGAGCTTCTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGACGACGAGGAGCAGGAGGTGCAGATGCTGGCC CCCTTGGAGAGCTGAGCTGCCCTGGTGG

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EST11458 6	--	--	---	---	---	CCACTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCCTCATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCAAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAAACAATCTATGAGCCAGGAGAGATACGTATCTCTGCAAGCCGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	---	---	---	CGGTCTCTCTCCAGGTATTGTGCAGAGGCGGAGATGACCTCTATGTCTCAGATGCATCCATAAG GCATTCTTTGAGGTGAGTACACCTTCCCACTCTTACGGTACAGAAAGAGATGCATGAACAGCA GGAACACGTGGAAGGCGCTGTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGGCCCT
EST62448 0	--	--	---	---	---	ACCTGGTGTGCTGTGGTGAACCTGGTCTCTTGGCAATTGCCGGCCCTCTGGGGCCCGTGG TCTCTCTGGTGTGGTGTGCTGGAGTCAACGGTCTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGGTCCGCCAGGTGGTGTCAACCCGACACAAAGGAGCGCGGTACCCCTGG CAATAT
EST36027 2	--	--	---	---	---	AGTGACTTCCAAAGGAAATGGCTACCCAACTTGGCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGGAAACCTGAAACAGG CTGTCAATCTACAGGGCTCTAATGATGTGAACCTGTTGCTGAGGGCAACAGAGTTTACACT GTCTTGTAGATGGCTGCTCTAAAGACAAATGAATGGGGAAGACAA
EST12274 0	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAAGTTTCTTGGTTCCTCAATAGAGCCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCTCTCATGACCAATATTTCTTCCCTCTTAGGATGAGGTGA TAGTAATGACCGATGGGTGAGAACTGTTCTGTCCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGGCAGATC
EST76807 EST44438 7	--	--	---	---	---	ATGCTAAGGGGATCGACATGAAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATCGGGACCTCAAGCTCGACTTCAAGGACGCTCT GCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGGTGGG
EST12839 3	--	--	---	---	---	TGCAAAACACACAAAATCTTCTCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACACAGAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAAGTATTACTTGAAGGAAACCTTGAATGTTATTCAACTGG ATTCCAGTAGGTTTCACTTACTTGAATATATGATACTTAGCTTAG
EST54419 8	--	--	---	---	---	CTTCTGCCTAATTTGAATGATATTGTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCTCGGAGATGATTGGGTTTAGCGTGGTGTGCTGTTGTCTACTA TAGTCCAAGTGAA

EST10398 2	--	--	--	---	---	---	TGCCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTACATTTGGGCTTGACCTTCCACACGGAGAAG CATTGTTTCTCGGGCCAAAGGATATCTACCAATAGTGTCTATTAGGCATTTG
EST36751 7	--	--	--	---	---	---	CCAAAGTCGTTCAATTTAGCTTTCAGGTTTAACTCGATTACTTTTCTATTCAAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40582	--	--	--	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAATTTCACTGGATGCTTAATAACAAATATTTACCTTTTGAAAAATAAATG AAGGATTTGACCTGCTCGCTCTGAAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGGCTCTCTACCCCTA
EST18288 3	--	--	--	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCAGAGGCTGTACAGGATGGAAGACTGGCTGCTCOCTGACGGAGCCAGTGTGG ACAGCACCTGGCTTTCACACCTAGTCCACTTCCAAGGTAAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	---	TTCCGCCAGCCCCCATCTTGGCACCTTGGTCCCTCAGGGGCAACCCCGGSCACTCACCGCTCT CGCTCTGGGTAACTCCGGCCGGCGCGCTCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCGGGCTTGCCAGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTTG
EST58707 7	--	--	--	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAATAACCTTAATCATTAATTGTTACAGGAGGCTTT AAGTTGAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCCCTAGAAGATACACGAGACCGA ATGATCAAATGGACATTCAGCAGGAACCTTCAOGATACCTGTCTGTTAGGCCAGGTTTATAGCA CACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTGAAGAACCCTT
EST74167 6	--	--	--	---	---	---	AGACCATGAAGGAGTTGAAGGCTTACAAATCGGAACCTGGAGGAACAACTGACCCGGTGGCGGAGG AGACGGGCACGGCTGTCAAGGAGCTGCAGGGCGGCGAGGCCGGCTGGCGCGGACATGGAGGA CGTGGCGGCGGCTGTGTGCACTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGC TGCGGGTGGGCTCGCTCCACTGCGCAAGCTGGGTAAAGGCTCTC
EST43211 8	--	--	--	---	---	---	CGCCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTGGCCAGACGCCAGGAGCTGGGGTGGG CCTCGCTCCACCTGCGCAAGCTGCATAAGCGGCTCTCGCGATGCCGATGACCTGCAGAGCGGCC TGGCAGTGTACAGGCGGCGGCGGAGGGCGGCGGCGGCTCAGCGCCATCCCGGAGGCGCTG GGGCCCTGTGTGAACAGGGCGGCTGGGGCGGCGGCTG
EST36770 4	--	--	--	---	---	---	TGTAGCCAAAGTCACTGCATCATCTTGGTGTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACCAACCAATATTACAGTTTGTGCTTCCATTATGATCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACCTGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAAGGCCCTAAAGAGGCTTATG

EST26021 1	--	--	--	---	---	TAATGTAAGCTCATCCACCAGAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTCTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGCAATTCCTGACGACATTCACCTACCAAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTTCTTTTGAACAAGCAAAAGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCCAATAGCTTCTTGTTCTACTTCTCTCCACAAGCCCCCAATTCACATTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTCCGAATCCTCCTCCTGAAAGTGGCCGGGTTTAACTGCTCATGACGCTGCGGCTGTGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGTTCTGCGTCATCCTTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCCAGGTCACACATTCACAGAAGAGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCTATGGGATTGACITTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATAGTGAAAAG GAAGCTTCAGCTCATGACAAATTTGAAGCTGACAAATTACAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCCAAGAGACCGGCTCAAGG ATCCAAAGGCCCAACTCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCCTCTTCTCTCCCTTGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACAGCAAGAGAAAGAGAGGCCCAAGAAAT CACAGGTGGGCACGTGCGGTCTACCGCCATCTCCCTTCTCACGGGAAATTTTCAGGGTAACT
EST74082 0	--	--	--	---	---	TCCAGGGTGGCTGGACCCCAAGGCCCAAGCTCTGCAGCAGGAGGACGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGCCCAAGGGGCCCAAGGCAGGGCACTGGCTTCAGCTGCTCAGCCCTGCTGCTGCTC CCAGATCACTGTCTCTTCTGCCATGGCCCTGTGGATGGCCCTCTGCCCCCTGCTGGCGCTGCTGGCCCTC TGGGGAACCTGACCCAGCCGCGAGCCTTTGTGAACCAACACCTGTGCG
EST45311 0	--	--	--	---	---	GCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTTCTCTATTAAAGTGAACATGACATCTTTTAGT GGATAGATGCACACAAACACAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAAACA CATTTTCTGCAAAATCACCTCTTTCATTTAAACAGCCCTTATTCAATGGCCCTTTTCTTTTCAGTAGTA CATACACATCTGTGTCATTGTGAAT

EST65258 8	---	---	---	---	---	TGCCCCATCAGCGGCGGAGACATGGCTTGCACACAGCTCTTGAGGATGTCACCAATTAACAGAAAT CCAGTTATTTCCACCCTCAAAATGACAGCCATGGCCGCGGGTCTCTGGGCTCGTCCGGGGG ACAGCTCCACTCTGACTGCGCACAGTCTTTGCATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG GTTAGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	---	---	---	---	---	ATGCAAGATGAAGGTGGACAGGGAGGAGAGGCCAACCTGTGATCCAGGCGCTGCAGATGTCGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 --	---	---	---	---	---	ATACTAGTACAAGTGGTAAATTTTGTACATTACACTAAATTAATAGCATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCTTAATGCTTATTTTAAATGACAGTGAAG TTTTTTTTCTCGAAGTGCCAGTATCCAGAGTTTGGTTTTTGAACAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTGGGGTTTTGGTGCATGCA
EST35879 9	---	---	---	---	---	GAGATCGGTGTGAGTATTAGGCATGGTACCTGTGATTCGCCAATCTTGTGCGTCCACCGATG GAACTGCCGGCAATCTGACACGTGTGCACCCAGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTGGAAGACACGCGGGATGGGGCAGGAGAGCTGCCCTGGATGAA
EST68308 5	---	---	---	---	---	GGAAAGAGATTTAAGAAGCTTGAATTTGGACAATTCGTGTTCTTGTGAGTGGGAAGAGTTTCATGTCTCT GCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAGGTAAAGAAAGTAGTATTTTTTA
EST54045 6	---	---	---	---	---	GGAATATTAATAATTTTAAATACCTCCATTTTGCCTTATCTCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTGATGTGGCAATTTGTTTCTTACAAAATCGGATGGAAATCT GTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
EST52908 0	---	---	---	---	---	ATCACAGGTCTCTGTCTCTGGCCATCATTTCTCTGGGAGAGATGGTGGTCTGCAAGCCCTTTGG CAATGTGAGATTGTATG
EST19590 --	---	---	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAAATGACATTGATGAGTGAAGATGTGGGCTCAGGAT GCCGGAATAATGAC
EST76136 --	---	---	---	---	---	TGAAGCTTCTGCCAGCTTGCTGCTGTTTCTAGGAGAACCCGCTCATACCTTTATCTATAGCCTTCCCC TAGGTCIT
EST58607 0	---	---	---	---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGAGAGAACAGGACAGCCACATGGCGGGGATGGCGGGGAGTTCTGGT TGCGGCCACGGCTGTGGCTCTGTTGTAACCGGTAGCCTTTGCGGTTGCGATGCTTAAACCTTTGTTCT TGGCCAAGGAGGGGGGTGGCCATGCTGAGATGATGAGTGGCC
						Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5..
- 16..The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

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